

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2003, 17:43:13 ; Search time 86 Seconds
(without alignments)
365.440 Million cell updates/sec

Title: US-09-995-593a-5

Perfect score: 1116

Sequence: 1 SGQFELILSMQNVNGELQN.....YACDQNGKTCMEGWGMSPEC 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1116	100.0	1010	20 AAW87896	Human JAGGED1 solu
2	1116	100.0	1036	18 AAW18351	Proliferation and
3	1116	100.0	1187	18 AAW18352	Proliferation and
4	1116	100.0	1208	19 AAW40827	Human Jagged prote
5	1116	100.0	1218	19 AAW44301	Human serrate 1.
6	1116	100.0	1218	20 AAW87894	Human JAGGED1 prot
7	1116	100.0	1218	23 ABB07822	Human notch agonis
8	1116	100.0	1218	24 ABB97800	Amino acid sequenc
9	1116	100.0	1218	24 ABB72569	Human Notch ligand

10	1116	100.0	1218	24 AAE34031	Human notch ligand
11	1116	100.0	1218	24 ABB55874	Human notch ligand
12	1109	99.4	296	24 ABB97797	Amino acid sequenc
13	1109	99.4	1218	17 AAW05833	Human Serrate-1 (H
14	1109	99.4	1218	21 AAY59597	Human Serrate prot
15	1109	99.4	1218	23 AAU84344	Protein JAG1 diffe
16	1102	98.7	1218	18 AAW18354	Proliferation and
17	1102	98.7	1218	24 AAE34030	Murine notch ligand
18	1102	98.7	1218	24 ABB55876	Mouse notch ligand
19	1073	96.1	192	18 AAW18350	Proliferation and
20	970	86.9	1193	17 AAW05835	Chick Serrate. Ga
21	970	86.9	1193	21 AAY59599	Human serrate 2 pr
22	652	58.4	214	19 AAW44297	Human serrate 2 pr
23	652	58.4	1055	19 AAW44298	Human serrate 2.
24	652	58.4	1212	19 AAW44299	Human notch ligand
25	652	58.4	1237	24 ABB55875	Human notch agonis
26	652	58.4	1238	23 ABB07823	Amino acid sequenc
27	652	58.4	1238	24 ABB97801	Human Notch ligand
28	652	58.4	1238	24 ABB72570	Human notch ligand
29	637	57.1	1237	24 AAE34032	Human JAGGED2 prot
30	584.5	52.4	1148	20 AAW87895	Sequence of a serr
31	447	40.1	1404	14 AAR38304	Serrate protein se
32	446	40.0	293	15 AAO27057	Drosophila Serrate
33	446	40.0	1404	21 AAY59600	Drosophila melanog
34	446	40.0	1404	22 ABB61998	Drosophila notch a
35	446	40.0	1404	23 ABB07827	C-Delta-1 polypept
36	433.5	38.8	727	18 AAW11719	C-Delta-1 polypept
37	433.5	38.8	740	18 AAW00876	Proliferation and
38	431	38.6	200	18 AAW18347	Truncated human de
39	431	38.6	200	20 AAW75493	Truncated human de
40	431	38.6	512	20 AAW75494	Proliferation and
41	431	38.6	520	18 AAW18348	Proliferation and
42	431	38.6	702	18 AAW18349	Truncated human de
43	431	38.6	702	20 AAW75495	Proliferation and
44	431	38.6	723	18 AAW18353	Human delta-1 prot
45	431	38.6	723	20 AAW94498	

ALIGNMENTS

RESULT 1

AAW87896

ID AAW87896 standard; Peptide; 1010 AA.

XX AC AAW87896;

XX 26-APR-1999 (first entry)

XX DE Human JAGGED1 soluble polypeptide.

XX JAGGED; JAGGED1; hJAGGED1; human; notch ligand; stem cell;
progenitor cell; haematopoiesis; cell differentiation;
Alagille syndrome; leukaemia; lymphoma; diagnosis; therapy.

XX OS Homo sapiens.

XX FH Key

FT Peptide Location/Qualifiers

FT Peptide 1..21

FT Protein /note= "signal peptide"

FT Protein /note= "mature protein"

FT Domain 185..239

FT Region /note= "Delta/Serrate/Lag-2 (DSL) domain"

FT Region 234..862

FT Region /note= "EGF-like repeat region"

XX WO9858958-A2.

XX 30-DEC-1998.

XX 25-JUN-1998;

XX 98WO-US13207.

25-JUN-1997; 97US-0882046.
(CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
(UNIW) UNIV WASHINGTON.
Hood L, Krantz ID, Li L, Spinner NB;
WPI; 1999-081220/07.
New Jagged peptides for inhibiting differentiation of progenitor
cells - also used for maintaining these cells in undifferentiated
state, e.g. for haematopoietic reconstitution
Claim 8; Page -: 101pp; English.
This is the amino acid sequence of a biologically active soluble
human JAGGED1 (hJAGGED1) polypeptide comprising amino acid residues
1-1010 of hJAGGED1 (see AAW87894). It was prepared by PCR
amplification (see AAV63759-60) of hJAGGED1 cDNA (see AAV63753) and
expression in CHO and BHK cells. hJAGGED1 is an activating ligand
for Notch protein that is expressed in bone marrow stromal cells.
A stromal cell line expressing hJAGGED1 permits survival and
proliferation of haematopoietic progenitor cells expressing Notch
but inhibits granulocyte differentiation. hJAGGED1 and active
peptides can be used (i) to inhibit differentiation of haematopoietic
progenitor cells (HPC), e.g. for subsequent production of blood cells
for transplantation or dendritic cells for immunotherapy, and (ii) to
maintain HPC in the undifferentiated state, particularly totipotent
cells or cells able to reconstitute the haematopoietic system, e.g.
in patients with leukaemia or lymphoma. Treated HPC, e.g. where
taken from a neonate, may be cryopreserved for many years, then
thawed for further expansion and differentiation. Optionally
JAGGED polypeptides are provided by transformed host cells.
(N.B. the amino acid sequence of the polypeptide of AAW87896 was
constructed from the full-length hJAGGED1 amino acid sequence given
in Fig1B of the specification).

Query Match 100.0%; Score 1116; DB 20; Length 1010;
Best Local Similarity 100.0%; Pred. No. 1e-102;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQGFLEILSMQNVNGLQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
DB 32 SQGFLEILSMQNVNGLQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 91
QY 61 CSFGSGSTPVIGGNTFNLSKASRGNDNRNRLVLPFSFAWPRSYTLVLEAWDSSNDTVQPSI 120
DB 92 CSFGSGSTPVIGGNTFNLSKASRGNDNRNRLVLPFSFAWPRSYTLVLEAWDSSNDTVQPSI 151
QY 121 IEKASHSGMINPSROWQTLKQNTGVAHFYQIRVTCDDYYVGGCNKFCRPRDDFGHYA 180
DB 152 IEKASHSGMINPSROWQTLKQNTGVAHFYQIRVTCDDYYVGGCNKFCRPRDDFGHYA 211

QY 181 CDQNGNKTCEMGWGPEC 198
DB 212 CDQNGNKTCEMGWGPEC 229

RESULT 2
AAW18351
ID AAW18351 standard; protein; 1036 AA.
XX
AC AAW18351;
XX
XX
DT 11-FEB-1998 (first entry)
XX
DE Proliferation and differentiation suppression polypeptide.
XX
KW Proliferation; differentiation; suppression; human; delta-1;
KW serrate-1; blood cell; neuron; leukaemia; malignant tumour;
KW immunosuppression.

XX Homo sapiens.
OS
XX
PN WO9719172-A1.
XX
PD 29-MAY-1997.
XX
PF 15-NOV-1996; 96WO-JP03356.
XX
PR 30-NOV-1995; 95JP-0311811.
PR 17-NOV-1995; 95JP-0299611.
XX
PA (ASAH) ASAH KASEI KOGYO KK.
XX
XX Itoh A, Sakano S;
XX WPI; 1997-298110/27.
XX
PT Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress
PT proliferation and differentiation of undifferentiated human blood
PT cells
XX
PS Claim 5; Page 66-71; 114pp; Japanese.
XX
CC The present sequence represents a polypeptide which suppresses
CC proliferation and differentiation of undifferentiated cells such
CC as neurons and blood cells. The polypeptide may be used for the
CC prevention and control of disorders involving undifferentiated
CC cells, such as leukaemia and malignant tumours, and improvement of
CC blood formation, e.g. after immunosuppression.
XX
SQ Sequence 1036 AA:
Query Match 100.0%; Score 1116; DB 18; Length 1036;
Best Local Similarity 100.0%; Pred. No. 1e-102;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQGFLEILSMQNVNGLQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
DB 1 SQGFLEILSMQNVNGLQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
QY 61 CSFGSGSTPVIGGNTFNLSKASRGNDNRNRLVLPFSFAWPRSYTLVLEAWDSSNDTVQPSI 120
DB 61 CSFGSGSTPVIGGNTFNLSKASRGNDNRNRLVLPFSFAWPRSYTLVLEAWDSSNDTVQPSI 120
QY 121 IEKASHSGMINPSROWQTLKQNTGVAHFYQIRVTCDDYYVGGCNKFCRPRDDFGHYA 180
DB 121 IEKASHSGMINPSROWQTLKQNTGVAHFYQIRVTCDDYYVGGCNKFCRPRDDFGHYA 180
QY 181 CDQNGNKTCEMGWGPEC 198
DB 181 CDQNGNKTCEMGWGPEC 198

RESULT 3
AAW18352
ID AAW18352 standard; protein; 1187 AA.
XX
AC AAW18352;
XX
DT 11-FEB-1998 (first entry)
XX
DE Proliferation and differentiation suppression polypeptide.
XX
KW Proliferation; differentiation; suppression; human; delta-1;
KW serrate-1; blood cell; neuron; leukaemia; malignant tumour;
KW immunosuppression.
XX
OS Homo sapiens.
XX
PN WO9719172-A1.
XX
PD 29-MAY-1997.

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XX 15-NOV-1996; 96WO-JP03356.
XX
PR 30-NOV-1995; 95JP-0311811.
PR 17-NOV-1995; 95JP-0299611.
XX
PA (ASAH ) ASahi KASEI KOGYO KK.
XX
PI Itoh A, Sakano S;
XX
DR WPI; 1997-298110/27.
XX
XX Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress
PT proliferation and differentiation of undifferentiated human blood
PT cells
XX
XX Claim 6; Page 71-76; 114pp; Japanese.
PS
XX The present sequence represents a polypeptide which suppresses
CC proliferation and differentiation of undifferentiated cells such
CC as neurons and blood cells. The polypeptide may be used for the
CC prevention and control of disorders involving undifferentiated
CC cells, such as leukaemia and malignant tumours, and improvement of
CC blood formation, e.g. after immunosuppression.
XX
XX Sequence 1187 AA;
SQ
Query Match 100.0%; Score 1116; DB 18; Length 1187;
Best Local Similarity 100.0%; Pred. No. 1.2e-102;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SQQFELEILSMQNVNGLQNGCCGARNPGDKRCKTRDECDTYFKVCLKEYQSRVTAGGP 60
Db 1 SQQFELEILSMQNVNGLQNGCCGARNPGDKRCKTRDECDTYFKVCLKEYQSRVTAGGP 60
Qy 61 CSFGSGSTPVIIGNTFNLKASRGNDNRNIVLPFSFAMPRSYTLLEAVDSSNDTVQPD SI 120
Db 61 CSFGSGSTPVIIGNTFNLKASRGNDNRNIVLPFSFAMPRSYTLLEAVDSSNDTVQPD SI 120
Qy 121 IEKASHSGMINPSRQWOTLKONTGVAHFQIRVTCDDYYGFCNKFRCPRDPFFGHYA 180
Db 121 IEKASHSGMINPSRQWOTLKONTGVAHFQIRVTCDDYYGFCNKFRCPRDPFFGHYA 180
Qy 181 CDQNGNKTCEMGWGMPEC 198
Db 181 CDQNGNKTCEMGWGMPEC 198
RESULT 4
AAW40827
ID AAW40827 standard; Protein; 1208 AA.
XX
AC AAW40827;
XX
XX 21-MAY-1998 (first entry)
XX
XX Human Jagged protein.
XX
XX Jagged; Notch; angiogenesis; endothelial cell; migration; human;
KW wound repair; vulnery; injury repair; signal transduction;
KW motor neurone disease; amyotrophic lateral sclerosis; polymyelitis;
KW diagnosis; therapy.
XX
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Peptide 1..11
FT Domain 175..220
FT /note= "DSL (Delta, Serrate, Lag-2 and Apx-1)
FT domain"
FT Region 224..852
FT /note= "EGF-like repeat region -containing 16

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FT Misc-difference 526 EGF repeats"
FT /note= "encoded by ANC"
FT Region 853..992
FT /note= "cysteine-rich region"
FT Domain 1058..1083
FT /note= "transmembrane domain"
FT Region 1084..1208
FT /note= "cytoplasmic region"
XX
XX WO9745143-A1.
XX
XX 04-DEC-1997.
XX
XX 30-MAY-1997; 97WO-US09407.
XX
XX 31-MAY-1996; 96US-0018841.
XX
XX (NAAM-) NAT AMERICAN RED CROSS.
XX (UYGE-) UNIV GENEVE.
XX
XX Maciag T, Montesano R, Pepper M, Wong MK, Zimrin AB;
XX
XX WPI; 1998-032340/03.
XX N-PSDB; AAV03674.
XX
XX New human Jagged protein - used to inhibit or promote angiogenesis
XX and to control migration of endothelial cells in injured blood
XX vessels
XX
XX Claim 2; Page 54-61; 81pp; English.
XX
XX This sequence comprises the human homologue of the rat Jagged
XX protein. Jagged is able to bind Notch protein and is involved in
XX endothelial cell (EC) migration and differentiation. The human
XX Jagged amino acid sequence was deduced from a human endothelial
XX cell cDNA (see AAV03674) induced by exposure to fibrin. Jagged
XX polypeptides can be expressed in host cell systems. A method for
XX treating or preventing disease by administering an agent that
XX (ant)agonises, inhibits, prevents, enhances or stimulates function
XX of the Notch or Jagged proteins is claimed, as well as a method for
XX affecting differentiation of mesoderm, endoderm, ectoderm and/or
XX neuroderm cells. When Jagged is applied to a micro-diameter blood
XX vessel from which ECs have been removed, damaged or reduced, it
XX decrease migrations of EC to the site, but when delivered to a
XX similar site on a large vessel it increases EC migration. Jagged
XX and its agonists are used to inhibit or prevent angiogenesis (where
XX associated with solid tumours, rheumatoid arthritis, inflammation,
XX or restenosis, particularly preventing angiogenesis from the vaso-
XX vasorum and promoting large vessel EC migration to repair the lumen
XX of large vessels). Anti-Jagged and Jagged antagonists (e.g.
XX antisense Jagged and Jagged mutants) are used to promote or enhance
XX angiogenesis, particularly for wound and injury repair, e.g. where
XX surgical, traumatic and/or caused by disease, e.g. diabetes-related
XX (all claimed). Angiogenesis can be modulated in vitro or in vivo
XX and expression of proteins by gene therapy is included. Modulation
XX of the Notch-Jagged signalling pathway may also be involved in
XX perinatal development and motor neurone diseases such as
XX amyotrophic lateral sclerosis, poliomyelitis etc.
XX
XX Sequence 1208 AA;

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Query Match 100.0%; Score 1116; DB 19; Length 1208;
Best Local Similarity 100.0%; Pred. No. 1.3e-102;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SQQFELEILSMQNVNGLQNGCCGARNPGDKRCKTRDECDTYFKVCLKEYQSRVTAGGP 60
Db 22 SQQFELEILSMQNVNGLQNGCCGARNPGDKRCKTRDECDTYFKVCLKEYQSRVTAGGP 81
Qy 61 CSFGSGSTPVIIGNTFNLKASRGNDNRNIVLPFSFAMPRSYTLLEAVDSSNDTVQPD SI 120
Db 82 CSFGSGSTPVIIGNTFNLKASRGNDNRNIVLPFSFAMPRSYTLLEAVDSSNDTVQPD SI 141

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Qy	61	CSFGSGSTPVIGGNTNLKASRGNDNRNRLVLPFSFAWPRSYTLLVEAWDSSNDTVQPDSI	121
Dd	92	CSFGSGSTPVIGGNTNLKASRGNDNRNRLVLPFSFAWPRSYTLLVEAWDSSNDTVQPDSI	151
Qy	121	IEKASHSGMINPSRQWTLKQNTGVVAHFYQIRVTCDYYGYGCGNKFCRPDRDDFFGHYA	180
Dd	152	IEKASHSGMINPSRQWTLKQNTGVVAHFYQIRVTCDYYGYGCGNKFCRPDRDDFFGHYA	211
Qy	181	CDQNGNKTCEGMWGPEC 198	
Dd	212	CDQNGNKTCEGMWGPEC 229	
RESULT 6			
ID	AAW87894	standard; Protein; 1218 AA.	
AC	AAW87894;		
DT	26-APR-1999	(first entry)	
DE	Human JAGGED1 protein.		
KW	JAGGED1; JAGGED1; human; notch ligand; stem cell;		
KW	progenitor cell; haematopoiesis; cell differentiation;		
KW	Alagille syndrome; leukaemia; lymphoma; diagnosis; therapy.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	Peptide	1..21	
FT	Protein	/note= "signal peptide"	
FT	Domain	22..1218	
FT	Region	/note= "mature protein"	
FT	Region	185..239	
FT	Region	/note= "Delta/Serrate/Lag-2 (DSL) domain"	
FT	Region	234..862	
FT	Region	/note= "EGF-like repeat region"	
FT	Domain	863..1012	
FT	Domain	/note= "cysteine-rich region"	
FT	Peptide	1077..1091	
FT	Peptide	/note= "transmembrane domain"	
FT	Peptide	188..204	
FT	Peptide	/note= "this peptide is specifically claimed in Claim 1"	
FT	Protein	178..240	
FT	Protein	/note= "this soluble peptide is specifically claimed in Claim 8"	
FT	Protein	1..1010	
FT	Protein	/note= "this soluble protein is specifically claimed in Claim 8"	
PN	WO9858958-A2.		
XX	30-DEC-1998.		
XX	25-JUN-1998;	98WO-US13207.	
XX	25-JUN-1997;	97US-0882046.	
XX	(CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.		
XX	(UNIW) UNIV WASHINGTON.		
PI	Hood L, Krantz ID, Li L, Spinner NB;		
XX	WPI; 1999-081220/07.		
DR	N-PSDB; AAV63753.		
XX	New Jagged peptides for inhibiting differentiation of progenitor		
PT	cells - also used for maintaining these cells in undifferentiated		
PT	state, e.g. for haematopoietic reconstitution		
XX	Claim 6; Fig 1A; 101pp; English.		

XX This is the amino acid sequence of human JAGGED1 (hJAGGED1), an
 CC activating ligand for Notch protein. hJAGGED1 is expressed in
 CC bone marrow stromal cells, and a stromal cell line expressing
 CC hJAGGED1 permits survival and proliferation of haematopoietic
 CC progenitor cells expressing Notch but inhibits granulocyte
 CC differentiation. A cDNA clone (see AAV63753) encoding hJAGGED1
 CC was obtained from a human bone marrow cDNA library. hJAGGED1
 CC polypeptides and biologically active peptides (see AA87896-98) are
 CC able (i) to inhibit differentiation of haematopoietic progenitor
 CC cells (HPC), e.g. for subsequent production of blood cells for
 CC transplantation or dendritic cells for immunotherapy, and (ii) to
 CC maintain HPC in the undifferentiated state, particularly totipotent
 CC cells or cells able to reconstitute the haematopoietic system, e.g.
 CC in patients with leukemia or lymphoma. Treated HPC, e.g. where
 CC taken from a neonate, may be cryopreserved for many years, then
 CC thawed for further expansion and differentiation. Optionally
 CC Jagged may be provided by cells transformed to express the
 CC membrane-bound protein. Antibodies raised against hJAGGED1 can
 CC be used in a method of diagnosing Alagille syndrome by detecting
 CC reduced expression of hJAGGED1 or expression of abnormal hJAGGED1.
 XX
 SQ Sequence 1218 AA;

Query Match 100.0%; Score 1116; DB 20; Length 1218;
 Best Local Similarity 100.0%; Pred. No. 1.3e-102;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGQFEILSMQNVNGLQNGCCGARNPDRKTRDECDTYFKVKLEYQSRVTAGGP 60
 DB 32 SGQFEILSMQNVNGLQNGCCGARNPDRKTRDECDTYFKVKLEYQSRVTAGGP 91
 QY 61 CSFGSGSTPVIGGNTFNKASRGNDRNRIVLPFSFAMPRSYTLLEAVDSSNDTVQDPSI 120
 DB 92 CSFGSGSTPVIGGNTFNKASRGNDRNRIVLPFSFAMPRSYTLLEAVDSSNDTVQDPSI 151
 QY 121 IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCNKFRCRPRDDFFGHYA 180
 DB 152 IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCNKFRCRPRDDFFGHYA 211
 QY 181 CDQNGNKTCEGWMGPEC 198
 DB 212 CDQNGNKTCEGWMGPEC 229

RESULT 7
 ABB07822
 ID ABB07822 standard; Protein; 1218 AA.
 XX ABB07822;
 XX 03-JUL-2002 (first entry)
 XX Human notch agonist ligand.
 DE Cell differentiation; notch; epidermis; cytostatic; dermatological;
 XX epithelial; skin; cancer; gamma secretase; human.
 XX Homo sapiens.
 OS
 XX W0200218544-A2.
 PN
 XX 07-MAR-2002.
 PD
 XX 31-AUG-2001; 2001WO-US7246.
 PF
 XX 31-AUG-2000; 2000US-229614P.
 PR
 XX (LOYO) UNIV LOYOLA CHICAGO.
 PA
 XX Nickoloff BJ, Miele L;
 PI WPI; 2002-339659/37.
 XX
 DR

XX Inducing differentiation of epithelial cell useful for inducing barrier
 PT formation within epithelium for treating psoriasis, sunburn, involves
 PT exogenously providing a source of a Notch agonist to the epithelial
 PT cell -
 XX
 XX Claim 10; Page 76-81; 101pp; English.
 PS
 XX The invention relates to a method of inducing differentiation of
 CC at least one epithelial cell. The method involves exogenously providing
 CC at least one source of at least one Notch agonist to at least one
 CC epithelial cell, whereby the Notch pathway is activated within at least
 CC one epithelial cell so that the differentiation of the cell is induced.
 CC Methods of producing differentiated epidermis; for assaying for genetic
 CC propensity of a patient to develop a disorder associated with epithelial
 CC barrier formation; for retarding progression of skin cancer and for
 CC diagnosing aggressive melanoma are also provided. The methods are useful
 CC for inducing differentiation of at least one epithelial cell e.g. a
 CC keratinocyte or a pre-malignant cell, in vivo or ex vivo. The method is
 CC useful for inducing differentiation of epithelial cell within cutaneous
 CC epithelial tissue or dermal equivalent, or within extracutaneous
 CC epithelium such as oral mucosal epithelial tissue, cornea epithelial
 CC tissue, gastrointestinal epithelia, urogenital epithelia, or respiratory
 CC epithelia. The methods are useful retarding the progression of skin
 CC cancer such as aggressive melanoma, aggressive cutaneous T-cell lymphoma
 CC (CTCL), aggressive squamous cell carcinoma, or aggressive basal cell
 CC carcinoma, by preferably administering an antagonist of the Notch
 CC pathway such as gamma secretase inhibitor. The present sequence
 CC represents a human notch agonist ligand.
 XX
 SQ Sequence 1218 AA;

Query Match 100.0%; Score 1116; DB 23; Length 1218;
 Best Local Similarity 100.0%; Pred. No. 1.3e-102;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGQFEILSMQNVNGLQNGCCGARNPDRKTRDECDTYFKVKLEYQSRVTAGGP 60
 DB 32 SGQFEILSMQNVNGLQNGCCGARNPDRKTRDECDTYFKVKLEYQSRVTAGGP 91
 QY 61 CSFGSGSTPVIGGNTFNKASRGNDRNRIVLPFSFAMPRSYTLLEAVDSSNDTVQDPSI 120
 DB 92 CSFGSGSTPVIGGNTFNKASRGNDRNRIVLPFSFAMPRSYTLLEAVDSSNDTVQDPSI 151
 QY 121 IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCNKFRCRPRDDFFGHYA 180
 DB 152 IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCNKFRCRPRDDFFGHYA 211
 QY 181 CDQNGNKTCEGWMGPEC 198
 DB 212 CDQNGNKTCEGWMGPEC 229

RESULT 8
 ABB97800
 ID ABB97800 standard; Protein; 1218 AA.
 XX ABB97800;
 XX 03-JUN-2003 (first entry)
 XX Amino acid sequence of human Jagged 1, a Notch ligand.
 DE
 XX
 XX MHC class II molecule; antigen presenting cell; APC; T cell;
 KW Notch signalling; T cell mediated disease; tumour; autoimmune disorder;
 KW rheumatoid arthritis; graft rejection; asthma; HIV; multiple sclerosis;
 KW diabetes; hepatitis; cardiac disease; dermatitis; periodontal disease;
 KW reproductive disorder; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; septic shock; stroke; Notch ligand; Jagged 1.
 XX
 OS Homo sapiens.
 XX
 XX W02003012111-A2.

PT Notch signaling in a cell of the immune system in the presence of
PT modulator

PS Disclosure; Fig 34; 184pp; English.

XX The present sequence is the protein sequence of the human Notch
CC ligand, Jagged 1. Jagged 1, its fragment, derivative, homologue,
CC analogue or allelic variant, or a polynucleotide encoding it,
CC can be used as a modulator of the Notch signalling pathway in the
CC method of the invention. The modulator may also comprise the Delta
CC Serrate lag2 (DSL) domain and at least one of the EGF-like repeat
CC motifs of a Notch ligand. The method detects modulators of Notch
CC signalling by monitoring the effect of a candidate modulator on
CC Notch signalling in a cell of the immune system, such as a T cell,
CC a B cell or an antigen presenting cell. The method is useful for
CC preparing a medicament for treating a disease or condition of, or
CC related to, the immune system, such as T-cell, B-cell or APC
CC mediated disease (all claimed), including cancer, acute and chronic
CC immune and autoimmune pathologies, infectious diseases,
CC inflammatory diseases, neurodegenerative diseases, alcohol-induced
CC hepatitis, other diseases related to angiogenesis, cardiovascular
CC conditions and pulmonary diseases.

XX Sequence 1218 AA;

Query Match 100.0%; Score 1116; DB 24; Length 1218;
Best Local Similarity 100.0%; Pred. No. 1.3e-102;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGQFELEILSMQNVNGLONGNCCGGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
DB 32 SGQFELEILSMQNVNGLONGNCCGGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 91
QY 61 CSFGSGSTPVIGGNTNFKASGRNDRNRIPLPSFAWPRSYTLLEAVDSSNDTVQDPSI 120
DB 92 CSFGSGSTPVIGGNTNFKASGRNDRNRIPLPSFAWPRSYTLLEAVDSSNDTVQDPSI 151
QY 121 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
DB 152 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 211
QY 181 CDQNGNKTCEGWMGPEC 198
DB 212 CDQNGNKTCEGWMGPEC 229

RESULT 10

AAE34031
ID AAE34031 standard; Protein; 1218 AA.

XX AAE34031;

XX 02-MAY-2003 (first entry)

XX Human notch ligand jagged 1 protein.

XX Human; drug screening; toxicology assay; signalling pathway;

XX notch ligand jagged 1; JAG1 protein.

XX Homo sapiens.

XX WO200290992-A2.

XX 14-NOV-2002.

XX 29-APR-2002; 2002WO-GB01946.

XX 04-MAY-2001; 2001GB-0011004.

XX (AXOR-) AXORDIA LTD.

XX Andrews P, Draper J, Walsh J;

DR WPI; 2003-120579/11.
DR N-PSDB; AAD52525.

XX Identifying biologically active agents comprises cloning transfected
PT cells into a cell array, exposing the array to an agent to be tested,
PT and detecting signals generated by a reporter molecule as a result of
PT exposure to the agent

XX Claim 16; Fig 5; 90pp; English.

XX The present invention relates to a novel screening method which enables
CC the identification of biologically active agents which mediate their
CC effect through the activation of genes. The method involves providing a
CC population of cells stably transfected with a nucleic acid encoding a
CC reporter molecule, cloning the transfected cells into a cell array,
CC exposing the array to at least one agent to be tested and detecting a
CC signal generated by the reporter molecule as a result of exposure to
CC the agent. The method is useful in identifying biologically active agents
CC and the genes through which the agents act, in screening potential drugs
CC for their ability to activate certain drug targets in a high-throughput
CC assay, in identifying relationships between signalling pathways and
CC specific signals that could be useful in eventually directing the
CC differentiation of embryonic stem cells and in toxicology assays by
CC testing for unwanted activation or inhibition of specific signalling
CC pathways. The present sequence is human notch ligand jagged 1 (JAG1)
CC protein used to illustrate the method of the invention.
CC Note: This sequence is encoded by a DNA containing translation
CC exceptions which alter the reading frame.

XX Sequence 1218 AA;

Query Match 100.0%; Score 1116; DB 24; Length 1218;
Best Local Similarity 100.0%; Pred. No. 1.3e-102;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGQFELEILSMQNVNGLONGNCCGGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
DB 32 SGQFELEILSMQNVNGLONGNCCGGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 91
QY 61 CSFGSGSTPVIGGNTNFKASGRNDRNRIPLPSFAWPRSYTLLEAVDSSNDTVQDPSI 120
DB 92 CSFGSGSTPVIGGNTNFKASGRNDRNRIPLPSFAWPRSYTLLEAVDSSNDTVQDPSI 151
QY 121 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
DB 152 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 211
QY 181 CDQNGNKTCEGWMGPEC 198
DB 212 CDQNGNKTCEGWMGPEC 229

RESULT 11

ABU55874
ID ABU55874 standard; Protein; 1218 AA.

XX ABU55874;

XX 25-MAR-2003 (first entry)

XX Human notch ligand jagged 1 protein.

XX Notch; Wnt; embryonic stem cell; embryogenesis; human;
KW differentiation; ligand; Parkinson's disease; Huntington's disease;
KW motor neuron disease; heart disease; diabetes; liver disease;
KW cirrhosis; renal disease; AIDS; acquired immunodeficiency syndrome.

XX Homo sapiens..

XX WO200277204-A2.

XX 03-OCT-2002.

QY	1	SGQFELEILSMQNVNGELQNGCCGARNPGDRKTRDECDTYFKVCLKEYQSRVTAGGP	60
Db	32	SGQFELEILSMQNVNGELQNGCCGARNPGDRKTRDECDTYFKVCLKEYQSRVTAGGP	91
QY	61	CSFGSGSTPVIGNTFNKASRGNDNRNIVLPFSFAWPRSYTLLVEAWDSSNDTVQPD	120
Db	92	CSFGSGSTPVIGNTFNKASRGNDNRNIVLPFSFAWPRSYTLLVEAWDSSNDTVQPD	151
QY	121	IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCGNKFCRPRDDFGHYA	180
Db	152	IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCGNKFCRPRDDFGHYA	211
QY	181	CDQNGNKTCTMEGWMGPEC	198
Db	212	CDQNGNKTCTMEGWMGPEC	229
RESULT 13			
AAW05833			
ID	AAW05833	standard; Protein; 1218 AA.	
XX	AC	AAW05833;	
XX	AC	AAW05833;	
DT	25-MAR-2003	(updated)	
DT	28-JAN-1997	(first entry)	
XX	Human Serrate-1 (HJL).		
XX	Serrate-1; human jagged-1; HJL; Notch; cell differentiation;		
KW	cell fate; central nervous system; cancer; tissue repair; therapy;		
KW	diagnosis; antibody.		
XX	Homo sapiens.		
XX	Key	Location/Qualifiers	
FT	Domain	1..1067	
FT	Peptide	/label= Extracellular_domain	
FT	Peptide	14..29	
FT	Domain	/label= Sig_peptide	
FT	Domain	185..229	
FT	Domain	/label= DSL	
FT	Domain	/note= "region of homology with Drosophila Delta and Serrate, predicted to mediate binding with Notch"	
FT	Domain	234..896	
FT	Domain	/label= ELR	
FT	Domain	/note= "epidermal growth factor-like repeat domain"	
FT	Region	234..264	
FT	Region	/label= ELR1	
FT	Region	265..299	
FT	Region	/label= ELR2	
FT	Region	300..339	
FT	Region	/label= ELR3	
FT	Region	340..377	
FT	Region	/label= ELR4	
FT	Region	378..415	
FT	Region	/label= ELR5	
FT	Region	416..453	
FT	Region	/label= ELR6	
FT	Region	454..490	
FT	Region	/label= ELR7	
FT	Region	491..528	
FT	Region	/label= ELR8	
FT	Region	529..566	
FT	Region	/label= ELR9	
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FT	Region	/label= Partial_EL	
FT	Region	599..632	
FT	Region	/label= Partial_EL	
FT	Region	633..670	
FT	Region	/label= ELR10	
FT	Region	671..708	

FT	Region	/label= ELR11	
FT	Region	709..747	
FT	Region	/label= ELR12	
FT	Region	748..785	
FT	Region	/label= ELR13	
FT	Region	786..823	
FT	Region	/label= ELR14	
FT	Region	824..862	
FT	Region	/label= ELR15	
FT	Region	863..879	
FT	Region	/label= Partial_EL	
FT	Region	880..896	
FT	Domain	/label= Partial_EL	
FT	Domain	1068..1089	
FT	Domain	/label= Transmembrane_domain	
FT	Domain	1090..1218	
FT	Domain	/label= Intracellular_domain	
XX	XX	WO9627610-A1.	
PN	XX	12-SEP-1996.	
PD	XX	07-MAR-1996; 96WO-US03172.	
XX	PF	07-MAR-1995; 95US-0400159.	
XX	PR	(IMCR) IMPERIAL CANCER RES TECHNOLOGY.	
XX	PA	(UYA) UNIV YALE.	
XX	PI	Ishhorowicz D, Henrique DMP, Lewis JH, Myat AM;	
XX	PI	Artavanis-tsakonas S, Mann RS, Gray GE;	
XX	DR	WPI; 1996-425379/42.	
DR	DR	N-PSDB; AAT40090.	
XX	XX	Vertebrate Serrate protein and related DNA - used to treat or prevent malignancies characterised by increased Notch activity.	
PT	PT	Claim 4; Page 95-98; 161pp; English.	
XX	XX	Human Serrate-1 (AAW05833) and human Serrate-2 (AAW05833) are ligands for the zygotic neurogenic locus Notch, and are believed to play a major role in determining cell fates (differentiation) in the central nervous system. Their amino acid sequences were deduced from cDNA clones (see also AAT40090-91) isolated from human foetal brain cDNA libraries. The proteins, antibodies raised to them, and encoding nucleic acids can be used in the detection of Serrate sequences and in the treatment of disorders of cell fate or differentiation, partic. cancer, nervous system disorders and in tissue repair or regeneration.	
CC	CC	(Updated on 25-MAR-2003 to correct PI field.)	
XX	SQ	Sequence 1218 AA;	
Query Match 99.4%; Score 1109; DB 17; Length 1218;			
Best Local Similarity 99.5%; Pred. No. 6.4e-102;			
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	1	SGQFELEILSMQNVNGELQNGCCGARNPGDRKTRDECDTYFKVCLKEYQSRVTAGGP	60
Db	32	SGQFELEILSMQNVNGELQNGCCGARNPGDRKTRDECDTYFKVCLKEYQSRVTAGGP	91
QY	61	CSFGSGSTPVIGNTFNKASRGNDNRNIVLPFSFAWPRSYTLLVEAWDSSNDTVQPD	120
Db	92	CSFGSGSTPVIGNTFNKASRGNDNRNIVLPFSFAWPRSYTLLVEAWDSSNDTVQPD	151
QY	121	IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCGNKFCRPRDDFGHYA	180
Db	152	IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCGNKFCRPRDDFGHYA	211
QY	181	CDQNGNKTCTMEGWMGPEC	198
Db	212	CDQNGNKTCTMEGWMGPEC	229

RESULT 14	
AAAY59597	
ID	AAAY59597 standard; Protein; 1218 AA.
XX	
AC	AAAY59597;
XX	
DT	05-APR-2000 (first entry)
XX	
DE	Human Serrate protein sequence.
XX	
KW	Serrate; cancerous condition; melanoma; lung cancer; breast cancer;
KW	nervous system disorder; infection; nutritional disease; therapy;
KW	cell proliferation promoter; tissue regeneration; human.
XX	
OS	Homo sapiens.
XX	
PN	US6004924-A.
XX	
PD	21-DEC-1999.
XX	
PF	06-MAR-1996; 96US-0611729.
XX	
PR	11-DEC-1991; 91US-0808458.
PR	14-SEP-1993; 93US-0121979.
PR	07-JUN-1994; 94US-0255102.
PR	07-MAR-1995; 95US-0400159.
XX	
PA	(IMCR) IMPERIAL CANCER RES TECHNOLOGY.
PA	(OYYA) UNIV YALE.
XX	
PI	Ish-Horowicz D, Henrique DMP, Myat AM, Fleming RJ;
PI	Artavanis-Tsakonas S, Gray GE, Mann RS, Lewis JH;
XX	
WPI	2000-105089/09.
DR	N-PSDB; AA249096.
XX	
PT	Purified Serrate proteins useful for treating neoplasias, nervous
PT	disorders and for promoting cell proliferation and tissue regeneration
PT	and repair .
XX	
PS	Claim 1; Fig 9; 114pp; English.
XX	
CC	This sequence represents a human serrate protein.
CC	The invention relates to purified vertebrate (mouse, chick, and human)
CC	Serrate proteins. The serrate proteins may be administered to treat a
CC	cancerous condition (e.g. melanoma, lung cancer and breast cancer) by
CC	preventing progression from a preneoplastic or nonmalignant state into a
CC	neoplastic or malignant state. It may also be used to treat nervous
CC	system disorders (such as lesions caused by infections, nutritional
CC	disease and toxic substances) and to promote cell proliferation and
CC	tissue regeneration and repair. The protein itself is administered to
CC	supplement a patient's own production of Serrate proteins (if levels of
CC	suppression are low) or to compensate for expression of inactive proteins
CC	due to genetic mutations. The protein may also be used in the production
CC	of antibodies against Serrate proteins which may be used to either down
CC	regulate Serrate activity or to detect Serrate proteins in samples (for
CC	example via enzyme-linked immunosorbent assay (ELISA)). The proteins may
CC	also be used to study Serrate expression and its role in metabolism and
CC	to assay for agents which modulate its expression and activity.
XX	
SQ	Sequence 1218 AA;
	Query Match 99.4%; Score 1109; DB 21; Length 1218;
	Best Local Similarity 99.5%; Pred. No. 6.4e-102;
	Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY	1 SCQFEELILSMQNYGELQNGCCGARNCGDRKCTRDECDTFYKVLKEYQSRVTAGGP 60
Db	32 SCQFEELILSMQNYGELQNGCCGARNCGDRKCTRDECDTFYKVLKEYQSRVTAGGP 91
QY	61 CSFGSGSTPVICGGTITFNLKASRGNDNRNRIVLPTFSFAWPRSYTLLVPAWDSNNDTVQPDSI 120

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Db 32 SGOFELEILSMQNVNGLQNGCCGGARNPCDRKTRDEC DTYFKVCLKEYQSRVTAGGP 91
QY 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNRIVLPEFAWPRSYTLLVEAWDSSNDTVQPD SI 120
Db 92 CSFGSGSTPVIGGNTFNLKASRGNDNRNRIVLPEFAWPRSYTLLVEAWDSSNDTVQPD SI 151
QY 121 IEKASHSGMINPSRQWOTLKONTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
Db 152 IEKASHSGMINPSRQWOTLKONTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 211
QY 181 CDQNGNKTCMEGWMGPEC 198
Db 212 CDQNGNKTCMEGWMGPEC 229

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Search completed: August 25, 2003, 17:52:28
 Job time : 87 secs

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GENERAL INFORMATION:
APPLICANT: Li, Linheng
APPLICANT: Hood, Leroy
APPLICANT: Krantz, Ian D.
APPLICANT: Spinner, Nancy B.
TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
TITLE OF INVENTION: Nucleic Acids and Methods of Use
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,046
FILING DATE: 25-JUN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UW 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1010 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-882-046-7

Query Match 100.0%; Score 1116; DB 3; Length 1010;
Best Local Similarity 100.0%; Pred. No. 2.5e-109;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQGFLEILSMQNVNGELQNGCCGARNPGDRKCTRDECDYFKVCLKEYQSRVTAGGP 60
Db 32 SQGFLEILSMQNVNGELQNGCCGARNPGDRKCTRDECDYFKVCLKEYQSRVTAGGP 91
QY 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNIRVLPFSFAWPRSYYTLLEAVDSSNDTVQPSI 120
Db 92 CSFGSGSTPVIGGNTFNLKASRGNDNRNIRVLPFSFAWPRSYYTLLEAVDSSNDTVQPSI 151
QY 121 IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
Db 152 IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 211
QY 181 CDQNGKNTCMEGWMGPEC 198
Db 212 CDQNGKNTCMEGWMGPEC 229

RESULT 3
US-09-068-740A-6
Sequence 6, Application US/09068740A
Patent No. 6337387
GENERAL INFORMATION:
APPLICANT: SAKANO, SEIJI
APPLICANT: ITOH, AKIRA
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8447
CURRENT APPLICATION NUMBER: US/09/068,740A
CURRENT FILING DATE: 1998-06-18
PRIOR FILING DATE: 1995-11-17
PRIOR FILING DATE: 1995-11-17

PRIOR APPLICATION NUMBER: JP 7-311811
PRIOR FILING DATE: 1995-11-30
PRIOR APPLICATION NUMBER: PCT/JP96/03356
PRIOR FILING DATE: 1996-11-15
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 1036
TYPE: PRT
ORGANISM: Homo sapiens
US-09-068-740A-6

Query Match 100.0%; Score 1116; DB 4; Length 1036;
Best Local Similarity 100.0%; Pred. No. 2.6e-109;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQGFLEILSMQNVNGELQNGCCGARNPGDRKCTRDECDYFKVCLKEYQSRVTAGGP 60
Db 1 SQGFLEILSMQNVNGELQNGCCGARNPGDRKCTRDECDYFKVCLKEYQSRVTAGGP 60
QY 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNIRVLPFSFAWPRSYYTLLEAVDSSNDTVQPSI 120
Db 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNIRVLPFSFAWPRSYYTLLEAVDSSNDTVQPSI 120
QY 121 IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
Db 121 IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
QY 181 CDQNGKNTCMEGWMGPEC 198
Db 181 CDQNGKNTCMEGWMGPEC 198

RESULT 4
US-09-068-740A-7
Sequence 7, Application US/09068740A
Patent No. 6337387
GENERAL INFORMATION:
APPLICANT: SAKANO, SEIJI
APPLICANT: ITOH, AKIRA
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8447
CURRENT APPLICATION NUMBER: US/09/068,740A
CURRENT FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: JP 7-299611
PRIOR FILING DATE: 1995-11-17
PRIOR APPLICATION NUMBER: JP 7-311811
PRIOR FILING DATE: 1995-11-30
PRIOR APPLICATION NUMBER: PCT/JP96/03356
PRIOR FILING DATE: 1996-11-15
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 1187
TYPE: PRT
ORGANISM: Homo sapiens
US-09-068-740A-7

Query Match 100.0%; Score 1116; DB 4; Length 1187;
Best Local Similarity 100.0%; Pred. No. 3.1e-109;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQGFLEILSMQNVNGELQNGCCGARNPGDRKCTRDECDYFKVCLKEYQSRVTAGGP 60
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QY 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNIRVLPFSFAWPRSYYTLLEAVDSSNDTVQPSI 120
Db 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNIRVLPFSFAWPRSYYTLLEAVDSSNDTVQPSI 120
QY 121 IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
Db 121 IEKASHSGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180

QY 1 SQQFEILSMQNVGELQNGCCGARNPGDRKCTRDECDFYFKVCLKEYQSRVTAGP 60
DB 22 SQQFEILSMQNVGELQNGCCGARNPGDRKCTRDECDFYFKVCLKEYQSRVTAGP 81
QY 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNRLVLPFSFAWPRSYTLLEAVDSSNDTVQPD SI 120
DB 82 CSFGSGSTPVIGGNTFNLKASRGNDNRNRLVLPFSFAWPRSYTLLEAVDSSNDTVQPD SI 141
QY 121 IEKASHGMINPSROWQTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
DB 142 IEKASHGMINPSROWQTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 201
QY 181 CDQNGNKTCMEGWMGPEC 198
DB 202 CDQNGNKTCMEGWMGPEC 219

RESULT 8

US-08-400-159-6
; Sequence 6, Application US/08400159
; Patent No. 5869282
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; APPLICANT: Henrique, Domingos M.P.
; APPLICANT: Lewis, Julian H.
; APPLICANT: Myat, Anna M.
; APPLICANT: Fleming, Robert J.
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Mann, Robert S.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
; TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400.159
FILING DATE: 07-MAR-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-400-159-6

Query Match 99.4%; Score 1109; DB 2; Length 1218;
Best Local Similarity 99.5%; Pred. No. 1.8e-108;
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SQQFEILSMQNVGELQNGCCGARNPGDRKCTRDECDFYFKVCLKEYQSRVTAGP 60
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QY 121 IEKASHGMINPSROWQTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
DB 152 IEKASHGMINPSROWQTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 211
QY 181 CDQNGNKTCMEGWMGPEC 198
DB 212 CDQNGNKTCMEGWMGPEC 229

RESULT 9

US-08-611-729A-6
; Sequence 6, Application US/08611729A
; Patent No. 6004924
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; APPLICANT: Henrique, Domingos M.P.
; APPLICANT: Lewis, Julian H.
; APPLICANT: Myat, Anna M.
; APPLICANT: Fleming, Robert J.
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Mann, Robert S.
; APPLICANT: Gray, Grace E.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
; TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611.729A
FILING DATE: 06-MAR-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-037
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1218 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-611-729A-6

Query Match 99.4%; Score 1109; DB 3; Length 1218;
Best Local Similarity 99.5%; Pred. No. 1.8e-108;
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SQQFEILSMQNVGELQNGCCGARNPGDRKCTRDECDFYFKVCLKEYQSRVTAGP 60
DB 32 SQQFEILSMQNVGELQNGCCGARNPGDRKCTRDECDFYFKVCLKEYQSRVTAGP 91
QY 61 CSFGSGSTPVIGGNTFNLKASRGNDNRNRLVLPFSFAWPRSYTLLEAVDSSNDTVQPD SI 120
DB 92 CSFGSGSTPVIGGNTFNLKASRGNDNRNRLVLPFSFAWPRSYTLLEAVDSSNDTVQPD SI 151

Qy 121 IEKASHGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCNKFRCRPRDDFFGHYA 180
Db 152 IEKASHGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCNKFRCRPRDDFFGHYA 211
Qy 181 CDQNGKTCMEGWMGPEC 198
Db 212 CDQNGKTCMEGWMGPEC 229

RESULT 10

US-08-882-046-5

; Sequence 5, Application US/08882046
; Patent No. 6136952

GENERAL INFORMATION:

APPLICANT: Li, Linheng
APPLICANT: Hood, Leroy
APPLICANT: Krantz, Ian D.
APPLICANT: Spinner, Nancy B.
TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
TITLE OF INVENTION: Nucleic Acids and Methods of Use
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/882.046
FILING DATE: 25-JUN-1997
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UW 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 1219 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-882-046-5

Query Match 99.4%; Score 1109; DB 3; Length 1219;

Best Local Similarity 98.5%; Pred. No. 1.8e-108;

Matches 195; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQQFEILSMQNVNGELQNGCCGARNPGDKRCTRDECDTYFKVCLKEYQSRVTAGGP 60
Db 32 SQQFEILSMQNVNGELQNGCCGARNPGDKRCTRDECDTYFKVCLKEYQSRVTAGGP 91
Qy 61 CSFGSGSTPVIGGNTFNLKASGRNDRNRIVLPFSFAMPRSYTLLEAVEADSSNDTVQPD SI 120
Db 92 CSFGSGSTPVIGGNTFNLKASGRNDRNRIVLPFSFAMPRSYTLLEAVEADSSNDTVQPD SI 151

Qy 121 IEKASHGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCNKFRCRPRDDFFGHYA 180
Db 152 IEKASHGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCNKFRCRPRDDFFGHYA 211

Qy 181 CDQNGKTCMEGWMGPEC 198

Db 212 CDQNGKTCMEGWMGPEC 229

RESULT 11

US-09-214-278-7

; Sequence 7, Application US/09214278

; Patent No. 6291210

GENERAL INFORMATION:

APPLICANT: Sakano, Seiji
APPLICANT: Itoh, Akira
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8576
CURRENT APPLICATION NUMBER: US/09/214, 278
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 1218
TYPE: PRT
ORGANISM: Homo sapiens
US-09-214-278-7

Query Match 99.1%; Score 1106; DB 3; Length 1218;

Best Local Similarity 99.5%; Pred. No. 3.7e-108;

Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SQQFEILSMQNVNGELQNGCCGARNPGDKRCTRDECDTYFKVCLKEYQSRVTAGGP 60
Db 32 SQQFEILSMQNVNGELQNGCCGARNPGDKRCTRDECDTYFKVCLKEYQSRVTAGGP 91

Qy 61 CSFGSGSTPVIGGNTFNLKASGRNDRNRIVLPFSFAMPRSYTLLEAVEADSSNDTVQPD SI 120
Db 92 CSFGSGSTPVIGGNTFNLKASGRNDRNRIVLPFSFAMPRSYTLLEAVEADSSNDTVQPD SI 151

Qy 121 IEKASHGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCNKFRCRPRDDFFGHYA 180
Db 152 IEKASHGMINPSRQWOTLKQNTGVAHFEYQIRVTCDDYYGFCNKFRCRPRDDFFGHYA 211

Qy 181 CDQNGKTCMEGWMGPEC 198

Db 212 CDQNGKTCMEGWMGPEC 229

RESULT 12

US-08-400-159-10

; Sequence 10, Application US/08400159

; Patent No. 5869282

GENERAL INFORMATION:

APPLICANT: Ish-Horowitz, David
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Myat, Anna M.
APPLICANT: Fleming, Robert J.
APPLICANT: Artavanis-Isakonas, Spyridon
APPLICANT: Mann, Robert S.
APPLICANT: Gray, Grace E.

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE

TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/400,159

FILING DATE: 07-MAR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1193 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-400-159-10

Query Match 86.9%; Score 970; DB 2; Length 1193;
Best Local Similarity 84.8%; Pred. No. 8.7e-94;
Matches 168; Conservative 14; Mismatches 16; Indels 0; Gaps 0;
QY 1-SGOFEEILSMONVNGELONGCCGARNPGDKCTRDECDTYFKVCLKEYOSRVTAGGP 60
DB 6 SGOFEEILSVQNVNGVLQNGCCDGRNPGDKCTRDECDTYFKVCLKEYOSRVTAGGP 65
QY 61 CSFGSGSTPVIIGNTFNLKASRGNDNRNRLVLPFSFAWPRSYTLVLEAWDSSNDTVOPDSI 120
DB 66 CSFGSKSTPVIIGNTFNLKASRNNEKNRIVIPFTFAWPRSYTLVLEAWDYNNDSTNPDR 125
QY 121 IEKASHGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYVGFGCNKFRCRDRDFFGHYA 180
DB 126 IEKASHGMINPSRQWTLKHTNTGAHFEYQIRVTCAEHYVGFGCNKFRCRDRDFFTHHT 185
QY 181 CDQNGNKTCEGWMGPEC 198
DB 186 CDQNGNKTCEGWTGPEC 203

RESULT 13

US-08-611-729A-10
Sequence 10, Application US/08611729A
Patent No. 6004924
GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Myat, Anna M.
APPLICANT: Fleming, Robert J.
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Mann, Robert S.
APPLICANT: Gray, Grace E.
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,729A
FILING DATE: 06-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-037

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1193 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-611-729A-10

Query Match 86.9%; Score 970; DB 3; Length 1193;
Best Local Similarity 84.8%; Pred. No. 8.7e-94;
Matches 168; Conservative 14; Mismatches 16; Indels 0; Gaps 0;
QY 1-SGOFEEILSMONVNGELONGCCGARNPGDKCTRDECDTYFKVCLKEYOSRVTAGGP 60
DB 6 SGOFEEILSVQNVNGVLQNGCCDGRNPGDKCTRDECDTYFKVCLKEYOSRVTAGGP 65
QY 61 CSFGSGSTPVIIGNTFNLKASRGNDNRNRLVLPFSFAWPRSYTLVLEAWDSSNDTVOPDSI 120
DB 66 CSFGSKSTPVIIGNTFNLKASRNNEKNRIVIPFTFAWPRSYTLVLEAWDYNNDSTNPDR 125
QY 121 IEKASHGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYVGFGCNKFRCRDRDFFGHYA 180
DB 126 IEKASHGMINPSRQWTLKHTNTGAHFEYQIRVTCAEHYVGFGCNKFRCRDRDFFTHHT 185
QY 181 CDQNGNKTCEGWMGPEC 198
DB 186 CDQNGNKTCEGWTGPEC 203

RESULT 14

US-08-882-046-6
Sequence 6, Application US/08882046
Patent No. 6136952
GENERAL INFORMATION:
APPLICANT: Li, Linheng
APPLICANT: Hood, Leroy
APPLICANT: Krantz, Ian D.
APPLICANT: Spinner, Nancy B.
TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
TITLE OF INVENTION: Nucleic Acids and Methods of Use
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,046
FILING DATE: 25-JUN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UW 2637
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1248 amino acids
TYPE: amino acid
TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-08-882-046-6

Query Match 58.5%; Score 653; DB 3; Length 1248;
Best Local Similarity 56.5%; Pred. No. 3.1e-60;
Matches 121; Conservative 27; Mismatches 48; Indels 18; Gaps 5;

QY 2 GQFEILSMQNYNGELQNGCC-GGARNPGRKTRDECDTYFKVCLKEYQSRVTAGGP 60
| | | | : : : | | | | : | | | | | | | | : : | |
Db 28 GFELQLSALRNNGELLSGACCDGRTTRAGCGRDECDTYVRVCLKEYQAKVTTPGP 87
| | | | : : : | | | | : | | | | | | | | : : | |
QY 61 CSFGSGSTPVIGNTNL-KASRGNDNR-----IVLPFSFAMPRSYTLLE 106
| | | | : : : | | | | : | | | | | | | | : : | |
Db 88 CSYGGATPVLGNSFYLPPAGAAGDRARARSRTGCHQDPLVVIPIPFQFAMPRSFLLIVE 147
| | | | : : : | | | | : | | | | | | | | : : | |
QY 107 AWDSSNDTVQPDSS--IIEKASHGSMINPSQWOTLKONTGVAHFEYQIRVTCDDYYGFG 164
| | | | : : : | | | | : | | | | | | | | : : | |
Db 148 AWDMDNTT-PDELLIERYSHAGMINPEDRWKSLHFSGHVAHLEQLQIRVRCDENYSAT 206
| | | | : : : | | | | : | | | | | | | | : : | |
QY 165 CNKFCRPRDFFGHYACDQNGKTCMEGWMGPEC 198
| | | | : : : | | | | : | | | | | | | | : : | |
Db 207 CNKFCRPRDFFGHYTCDOYGNKACMDGWMGKEC 240
| | | | : : : | | | | : | | | | | | | | : : | |

RESULT 15

US-09-214-278-1
; Sequence 1, Application US/09214278
; Patent No. 6291210
; GENERAL INFORMATION:
; APPLICANT: Sakano, Seiji
; APPLICANT: Itoh, Akira
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8576
; CURRENT APPLICATION NUMBER: US/09/214,278
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-278-1

Query Match 58.4%; Score 652; DB 3; Length 214;
Best Local Similarity 55.4%; Pred. No. 3.9e-61;
Matches 118; Conservative 31; Mismatches 48; Indels 16; Gaps 4;

QY 2 GQFEILSMQNYNGELQNGCC-GGARNPGRKTRDECDTYFKVCLKEYQSRVTAGGP 60
| | | | : : : | | | | : | | | | | | | | : : | |
Db 2 GFELQLSALRNNGELLSGACCDGRTTRAGCGRDECDTYVRVCLKEYQAKVTTPGP 61
| | | | : : : | | | | : | | | | | | | | : : | |
QY 61 CSFGSGSTPVIGNTNL-----KASRGNDNR--RIVLPFSFAMPRSYTLLE 106
| | | | : : : | | | | : | | | | | | | | : : | |
Db 62 CSYGGATPVLGNSFYLPPAGAAGDRARARAGQDPLVVIPIPFQFAMPRSFLLIVE 121
| | | | : : : | | | | : | | | | | | | | : : | |
QY 107 AWDSSNDTV-QPDSSIIIEKASHGSMINPSQWOTLKONTGVAHFEYQIRVTCDDYYGFGC 165
| | | | : : : | | | | : | | | | | | | | : : | |
Db 122 AWDMDNTTNEELLIERVSHAGMINPEDRWKSLHFSGHVAHLEQLQIRVRCDENYSATC 181
| | | | : : : | | | | : | | | | | | | | : : | |
QY 166 NKFCRPRDFFGHYACDQNGKTCMEGWMGPEC 198
| | | | : : : | | | | : | | | | | | | | : : | |
Db 182 NKFCRPRDFFGHYTCDOYGNKACMDGWMGKEC 214
| | | | : : : | | | | : | | | | | | | | : : | |

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Job time : 31 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2003, 17:52:33 ; Search time 57 Seconds
(without alignments)
458.393 Million cell updates/sec

Title: US-09-995-593A-5
Perfect score: 1116
Sequence: 1 SQGFELLSQNVNGELQN.....YACDQNGKTCMEGWMGPEC 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 497079 seqs, 131961718 residues .

Total number of hits satisfying chosen parameters: 497079

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1116	100.0	198	10	US-09-995-593A-5
2	1116	100.0	1036	10	US-09-995-593A-6
3	1116	100.0	1187	10	US-09-995-593A-7
4	1116	100.0	1218	10	US-09-995-593A-11
5	1116	100.0	1218	10	US-09-944-849-3
6	1109	99.4	1208	15	US-10-213-329-1
7	1106	99.1	1218	9	US-09-855-722-7
8	1106	99.1	1218	15	US-10-219-248-7
9	1106	99.1	1218	15	US-10-219-247-7
10	1102	98.7	1218	15	US-10-281-478-7
11	652	58.4	214	9	US-09-855-722-1
12	652	58.4	214	15	US-10-219-248-1
13	652	58.4	214	15	US-10-219-247-1
14	652	58.4	1055	9	US-09-855-722-2
15	652	58.4	1055	15	US-10-219-248-2

16	652	58.4	1055	15	US-10-219-247-2	Sequence 2, Appli
17	652	58.4	1212	9	US-09-855-722-3	Sequence 3, Appli
18	652	58.4	1212	15	US-10-219-248-3	Sequence 3, Appli
19	652	58.4	1212	15	US-10-219-247-3	Sequence 3, Appli
20	652	58.4	1238	9	US-09-855-722-5	Sequence 5, Appli
21	652	58.4	1238	10	US-09-944-849-4	Sequence 4, Appli
22	652	58.4	1238	15	US-10-219-248-5	Sequence 5, Appli
23	652	58.4	1238	15	US-10-219-247-5	Sequence 5, Appli
24	446	40.0	1404	10	US-09-944-849-8	Sequence 8, Appli
25	433.5	38.8	728	10	US-09-908-322-2	Sequence 2, Appli
26	433.5	38.8	728	11	US-09-783-931-2	Sequence 2, Appli
27	431	38.6	520	10	US-09-995-593A-3	Sequence 3, Appli
28	431	38.6	702	10	US-09-995-593A-4	Sequence 4, Appli
29	431	38.6	723	9	US-09-828-366-21	Sequence 21, Appli
30	431	38.6	723	10	US-09-995-593A-9	Sequence 9, Appli
31	431	38.6	723	12	US-10-137-870-346	Sequence 346, App
32	431	38.6	723	12	US-10-140-018-346	Sequence 346, App
33	431	38.6	723	12	US-10-140-021-346	Sequence 346, App
34	431	38.6	723	12	US-10-140-274-346	Sequence 346, App
35	431	38.6	723	12	US-10-140-471-346	Sequence 346, App
36	431	38.6	723	12	US-10-140-807-346	Sequence 346, App
37	431	38.6	723	12	US-10-140-922-346	Sequence 346, App
38	431	38.6	723	12	US-10-140-924-346	Sequence 346, App
39	431	38.6	723	12	US-10-140-926-346	Sequence 346, App
40	431	38.6	723	12	US-10-141-698-346	Sequence 346, App
41	431	38.6	723	12	US-10-141-702-346	Sequence 346, App
42	431	38.6	723	12	US-10-141-704-346	Sequence 346, App
43	431	38.6	723	12	US-10-142-421-346	Sequence 346, App
44	431	38.6	723	12	US-10-142-432-346	Sequence 346, App
45	431	38.6	723	12	US-10-142-767-346	Sequence 346, App

ALIGNMENTS

RESULT 1
US-09-995-593A-5
; Sequence 5, Application US/09995593A
; Patent No. US20020128197A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, AKIRA
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP8447DIV
; CURRENT APPLICATION NUMBER: US/09/995,593A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 09/068,740
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: JP-7-299611
; PRIOR FILING DATE: 1995-11-17
; PRIOR APPLICATION NUMBER: JP 7-311811
; PRIOR FILING DATE: 1995-11-30
; PRIOR APPLICATION NUMBER: PCT/JP96/03356
; PRIOR FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-995-593A-5

Query Match .100.0%; Score 1116; DB 10; Length 198;
Best Local Similarity 100.0%; Pred. No. 3.4e-111;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQGFELLSQNVNGELQNGCCGARNPGDKTRDECDFYFKVCLKEYQSRYTAGP 60
DB 1 SQGFELLSQNVNGELQNGCCGARNPGDKTRDECDFYFKVCLKEYQSRYTAGP 60
QY 61 CSFGSGSPVIGGNTFNLKASRGNDNRNIVLPFSAWPRSYTLLVEANDSSNDTVQPSI 120
DB 61 CSFGSGSPVIGGNTFNLKASRGNDNRNIVLPFSAWPRSYTLLVEANDSSNDTVQPSI 120

QY 121 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFCNKFCRPRDDFFGHYA 180
|||||
Db 121 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFCNKFCRPRDDFFGHYA 180
|||||
QY 181 CDQNGKNTCMEGWMGPEC 198
|||||
Db 181 CDQNGKNTCMEGWMGPEC 198
|||||

RESULT 2

US-09-995-593A-6
; Sequence 6, Application US/09995593A
; Patent No. US20020128197A1
; GENERAL INFORMATION:
; APPLICANT: SAKANO, SEIJI
; APPLICANT: ITOH, AKIRA
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP8447DIV
; CURRENT APPLICATION NUMBER: US/09/995,593A
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 09/068,740
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: JP 7-299611
; PRIOR FILING DATE: 1995-11-17
; PRIOR APPLICATION NUMBER: JP 7-311811
; PRIOR FILING DATE: 1995-11-30
; PRIOR APPLICATION NUMBER: PCT/JP96/03356
; PRIOR FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-995-593A-6

Query Match 100.0%; Score 1116; DB 10; Length 1036;
Best Local Similarity 100.0%; Pred. No. 2.8e-110;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGQFEILSMQNVNGLQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
|||||
Db 1 SGQFEILSMQNVNGLQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
|||||
QY 61 CSFGSGSTPVIGGNTFNKASRGNDNRNIRIVLPFSFAPRSYTLLEAVDSSNDTVQDSI 120
|||||
Db 61 CSFGSGSTPVIGGNTFNKASRGNDNRNIRIVLPFSFAPRSYTLLEAVDSSNDTVQDSI 120
|||||
QY 121 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFCNKFCRPRDDFFGHYA 180
|||||
Db 121 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFCNKFCRPRDDFFGHYA 180
|||||
QY 181 CDQNGKNTCMEGWMGPEC 198
|||||
Db 181 CDQNGKNTCMEGWMGPEC 198
|||||

RESULT 3

US-09-995-593A-7
; Sequence 7, Application US/09995593A
; Patent No. US20020128197A1
; GENERAL INFORMATION:
; APPLICANT: SAKANO, SEIJI
; APPLICANT: ITOH, AKIRA
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP8447DIV
; CURRENT APPLICATION NUMBER: US/09/995,593A
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 09/068,740
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: JP 7-299611
; PRIOR FILING DATE: 1995-11-17

; PRIOR APPLICATION NUMBER: JP 7-311811
; PRIOR FILING DATE: 1995-11-30
; PRIOR APPLICATION NUMBER: PCT/JP96/03356
; PRIOR FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-995-593A-7

Query Match 100.0%; Score 1116; DB 10; Length 1187;
Best Local Similarity 100.0%; Pred. No. 3.3e-110;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGQFEILSMQNVNGLQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
|||||
Db 1 SGQFEILSMQNVNGLQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
|||||
QY 61 CSFGSGSTPVIGGNTFNKASRGNDNRNIRIVLPFSFAPRSYTLLEAVDSSNDTVQDSI 120
|||||
Db 61 CSFGSGSTPVIGGNTFNKASRGNDNRNIRIVLPFSFAPRSYTLLEAVDSSNDTVQDSI 120
|||||
QY 121 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFCNKFCRPRDDFFGHYA 180
|||||
Db 121 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFCNKFCRPRDDFFGHYA 180
|||||
QY 181 CDQNGKNTCMEGWMGPEC 198
|||||
Db 181 CDQNGKNTCMEGWMGPEC 198
|||||

RESULT 4

US-09-995-593A-11
; Sequence 11, Application US/09995593A
; Patent No. US20020128197A1
; GENERAL INFORMATION:
; APPLICANT: SAKANO, SEIJI
; APPLICANT: ITOH, AKIRA
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP8447DIV
; CURRENT APPLICATION NUMBER: US/09/995,593A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 09/068,740
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: JP 7-299611
; PRIOR FILING DATE: 1995-11-17
; PRIOR APPLICATION NUMBER: JP 7-311811
; PRIOR FILING DATE: 1995-11-30
; PRIOR APPLICATION NUMBER: PCT/JP96/03356
; PRIOR FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 1218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-995-593A-11

Query Match 100.0%; Score 1116; DB 10; Length 1218;
Best Local Similarity 100.0%; Pred. No. 3.4e-110;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGQFEILSMQNVNGLQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
|||||
Db 32 SGQFEILSMQNVNGLQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 91
|||||
QY 61 CSFGSGSTPVIGGNTFNKASRGNDNRNIRIVLPFSFAPRSYTLLEAVDSSNDTVQDSI 120
|||||
Db 92 CSFGSGSTPVIGGNTFNKASRGNDNRNIRIVLPFSFAPRSYTLLEAVDSSNDTVQDSI 151
|||||
QY 121 IEKASHSGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFCNKFCRPRDDFFGHYA 180
|||||

Db 152 IEKASHGMINPSRQWOTLKONTGVAHFEYQIRVTCDDYYGFCNKFRCRPRDDFFGHYA 211
Qy 181 CDQNGNKTCEGWMGPEC 198
Db 212 CDQNGNKTCEGWMGPEC 229

RESULT 5

US-09-944-849-3

; Sequence 3, Application US/09944849

; Patent No. US20020151487A1

; GENERAL INFORMATION:

; APPLICANT: Nickoloff, Brian

; APPLICANT: Miele, Lucio

; TITLE OF INVENTION: METHOD AND REAGENTS FOR EPITHELIAL BARRIER FORMATION AND TREATMEN

; TITLE OF INVENTION: MALIGNANT AND BENIGN SKIN DISORDERS BY MODULATING THE NOTCH PATH

; CURRENT APPLICATION NUMBER: US/09/944,849

; CURRENT FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: US 60/229,614

; PRIOR FILING DATE: 2000-08-31

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 1218

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-944-849-3

Query Match 100.0%; Score 1116; DB 10; Length 1218;
Best Local Similarity 100.0%; Pred. No. 3.4e-110;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQQFELEILSMQNVNGELQNGCCGARNPGDKRCKTRDECPTYFKVCLKEYQSRVTAGGP 60
Db 32 SQQFELEILSMQNVNGELQNGCCGARNPGDKRCKTRDECPTYFKVCLKEYQSRVTAGGP 91
Qy 61 CSFGSGSTPVIGGNTFNLKASGRNDRNRIPLPFSFAMPRSYTLLEAVDSSNDTVQDPSI 120
Db 92 CSFGSGSTPVIGGNTFNLKASGRNDRNRIPLPFSFAMPRSYTLLEAVDSSNDTVQDPSI 151
Qy 121 IEKASHGMINPSRQWOTLKONTGVAHFEYQIRVTCDDYYGFCNKFRCRPRDDFFGHYA 180
Db 152 IEKASHGMINPSRQWOTLKONTGVAHFEYQIRVTCDDYYGFCNKFRCRPRDDFFGHYA 211
Qy 181 CDQNGNKTCEGWMGPEC 198
Db 212 CDQNGNKTCEGWMGPEC 229

RESULT 6

US-10-213-329-1

; Sequence 1, Application US/10213329

; Publication No. US20030083465A1

; GENERAL INFORMATION:

; APPLICANT: Zimrin, Ann B.

; APPLICANT: Maciag, Thomas

; APPLICANT: Wong, Michael K.K.

; APPLICANT: Pepper, Michael S.

; APPLICANT: Montesano, Roberto

; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS

; TITLE OF INVENTION: BASED ON JAGGED/NOTCH PROTEINS AND NUCLEIC ACIDS

; FILE REFERENCE: 0036-101

; CURRENT APPLICATION NUMBER: US/10/213,329

; CURRENT FILING DATE: 2002-08-06

; PRIOR APPLICATION NUMBER: US/09/199,865

; PRIOR FILING DATE: 1998-11-25

; PRIOR APPLICATION NUMBER: 60/018,841

; PRIOR FILING DATE: 1996-05-31

; PRIOR APPLICATION NUMBER: PCT/US97/09407

; PRIOR FILING DATE: 1997-05-30

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 1208

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-213-329-1

Query Match 99.4%; Score 1109; DB 15; Length 1208;
Best Local Similarity 99.5%; Pred. No. 1.9e-109;
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SQQFELEILSMQNVNGELQNGCCGARNPGDKRCKTRDECPTYFKVCLKEYQSRVTAGGP 60
Db 22 SQQFELEILSMQNVNGELQNGCCGARNPGDKRCKTRDECPTYFKVCLKEYQSRVTAGGP 81
Qy 61 CSFGSGSTPVIGGNTFNLKASGRNDRNRIPLPFSFAMPRSYTLLEAVDSSNDTVQDPSI 120
Db 82 CSFGSGSTPVIGGNTFNLKASGRNDRNRIPLPFSFAMPRSYTLLEAVDSSNDTVQDPSI 141
Qy 121 IEKASHGMINPSRQWOTLKONTGVAHFEYQIRVTCDDYYGFCNKFRCRPRDDFFGHYA 180
Db 142 IEKASHGMINPSRQWOTLKONTGVAHFEYQIRVTCDDYYGFCNKFRCRPRDDFFGHYA 201
Qy 181 CDQNGNKTCEGWMGPEC 198
Db 202 CDQNGNKTCEGWMGPEC 219

RESULT 7

US-09-855-722-7

; Sequence 7, Application US/09855722

; Patent No. US20020049306A1

; GENERAL INFORMATION:

; APPLICANT: Sakano, Seiji

; APPLICANT: Itoh, Akira

; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE

; FILE REFERENCE: KP-8576

; CURRENT APPLICATION NUMBER: US/09/855,722

; CURRENT FILING DATE: 2001-05-16

; PRIOR APPLICATION NUMBER: 09/214,278

; PRIOR FILING DATE: 1999-01-26

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 1218

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-855-722-7

Query Match 99.1%; Score 1106; DB 9; Length 1218;
Best Local Similarity 99.5%; Pred. No. 4e-109;
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SQQFELEILSMQNVNGELQNGCCGARNPGDKRCKTRDECPTYFKVCLKEYQSRVTAGGP 60
Db 32 SQQFELEILSMQNVNGELQNGCCGARNPGDKRCKTRDESPTYFKVCLKEYQSRVTAGGP 91
Qy 61 CSFGSGSTPVIGGNTFNLKASGRNDRNRIPLPFSFAMPRSYTLLEAVDSSNDTVQDPSI 120
Db 92 CSFGSGSTPVIGGNTFNLKASGRNDRNRIPLPFSFAMPRSYTLLEAVDSSNDTVQDPSI 151
Qy 121 IEKASHGMINPSRQWOTLKONTGVAHFEYQIRVTCDDYYGFCNKFRCRPRDDFFGHYA 180
Db 152 IEKASHGMINPSRQWOTLKONTGVAHFEYQIRVTCDDYYGFCNKFRCRPRDDFFGHYA 211
Qy 181 CDQNGNKTCEGWMGPEC 198
Db 212 CDQNGNKTCEGWMGPEC 229

RESULT 8

US-10-219-248-7

; Sequence 7, Application US/10219248

Publication No. US20030022368A1
GENERAL INFORMATION:
APPLICANT: Sakano, Seiji
APPLICANT: Itoh, Akira
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8576
CURRENT APPLICATION NUMBER: US/10/219,248
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US/09/214,278
PRIOR FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 1218
TYPE: PRT
ORGANISM: Homo sapiens
US-10-219-248-7

Query Match 99.1%; Score 1106; DB 15; Length 1218;
Best Local Similarity 99.5%; Pred. No. 4e-109;
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SGQFEILSMQNVNGELQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
DB 32 SGQFEILSMQNVNGELQNGCCGARNPGDRKCTRDESDTYFKVCLKEYQSRVTAGGP 91
QY 61 CSFGSGSTPVIGGNTFNKASRGNDNRNRLVLPFSFAPRSTYLLVEAWDSSNDTVQPSI 120
DB 92 CSFGSGSTPVIGGNTFNKASRGNDNRNRLVLPFSFAPRSTYLLVEAWDSSNDTVQPSI 151
QY 121 IEKASHGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
DB 152 IEKASHGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 211
QY 181 CDQNGNKTCEGWMGPEC 198
DB 212 CDQNGNKTCEGWMGPEC 229

RESULT 9
US-10-219-247-7
Sequence 7, Application US/10219247
Publication No. US20030032781A1
GENERAL INFORMATION:
APPLICANT: Sakano, Seiji
APPLICANT: Itoh, Akira
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8576
CURRENT APPLICATION NUMBER: US/10/219,247
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US/09/855,722
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/214,278
PRIOR FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 1218
TYPE: PRT
ORGANISM: Homo sapiens
US-10-219-247-7

Query Match 99.1%; Score 1106; DB 15; Length 1218;
Best Local Similarity 99.5%; Pred. No. 4e-109;
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SGQFEILSMQNVNGELQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
DB 32 SGQFEILSMQNVNGELQNGCCGARNPGDRKCTRDESDTYFKVCLKEYQSRVTAGGP 91
QY 61 CSFGSGSTPVIGGNTFNKASRGNDNRNRLVLPFSFAPRSTYLLVEAWDSSNDTVQPSI 120
DB 92 CSFGSGSTPVIGGNTFNKASRGNDNRNRLVLPFSFAPRSTYLLVEAWDSSNDTVQPSI 151

QY 121 IEKASHGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
DB 152 IEKASHGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 211
QY 181 CDQNGNKTCEGWMGPEC 198
DB 212 CDQNGNKTCEGWMGPEC 229
RESULT 10
US-10-281-478-7
Sequence 7, Application US/10281478
Publication No. US20030108959A1
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Johnson, Richard S.
APPLICANT: Guo, Lin
APPLICANT: Mahinkar, Rajeev M.
APPLICANT: Peschon, Jacques J.
APPLICANT: Black, Roy A.
TITLE OF INVENTION: TREATING DISEASES MEDIATED BY METALLOPROTEASE-SHED PROTEINS
FILE REFERENCE: 3327-A
CURRENT APPLICATION NUMBER: US/10/281,478
CURRENT FILING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 158
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 1218
TYPE: PRT
ORGANISM: Mus musculus
US-10-281-478-7

Query Match 98.7%; Score 1102; DB 15; Length 1218;
Best Local Similarity 97.5%; Pred. No. 1.1e-108;
Matches 193; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 SGQFEILSMQNVNGELQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 60
DB 32 SGQFEILSMQNVNGELQNGCCGARNPGDRKCTRDECDTYFKVCLKEYQSRVTAGGP 91
QY 61 CSFGSGSTPVIGGNTFNKASRGNDNRNRLVLPFSFAPRSTYLLVEAWDSSNDTVQPSI 120
DB 92 CSFGSGSTPVIGGNTFNKASRGNDNRNRLVLPFSFAPRSTYLLVEAWDSSNDTVQPSI 151
QY 121 IEKASHGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 180
DB 152 IEKASHGMINPSRQWTLKQNTGVAHFEYQIRVTCDDYYGFGCNKFCRPRDDFFGHYA 211
QY 181 CDQNGNKTCEGWMGPEC 198
DB 212 CDQNGNKTCEGWMGPEC 229

RESULT 11
US-09-855-722-1
Sequence 1, Application US/09855722
Patent No. US20020049306A1
GENERAL INFORMATION:
APPLICANT: Sakano, Seiji
APPLICANT: Itoh, Akira
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8576
CURRENT APPLICATION NUMBER: US/09/855,722
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/214,278
PRIOR FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapiens

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2003, 17:50:28 ; Search time 40 Seconds
(without alignments)
476.035 Million cell updates/sec

Title: US-09-995-593A-5

Perfect score: 1116

Sequence: 1 SGQFELEILSMQNVNGELQN.....YACDQNGNKTCMEGWMGPEC 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1044.5	93.6	1220	2 A56136	jagged protein prec
2	446	40.0	1408	2 S16148	gene serrate prote
3	433.5	38.8	728	2 I50719	C-Delta-1 - chicke
4	423	37.9	833	2 S19087	gene delta protein
5	420	37.6	832	2 A31246	neurogenic protein
6	420	37.6	880	2 S00670	neurogenic repetit
7	419.5	37.6	685	2 JC7570	Delta-4 protein -
8	419.5	37.6	722	2 I48324	DELTA-like 1 - mou
9	410.5	36.8	686	2 JC7569	delta-4 protein -
10	125.5	11.2	379	2 T16213	APX-1 protein homo
11	118.5	10.6	513	2 D88991	protein apx-1 (imp
12	114	10.2	402	2 S42367	lag-2 protein - Ca
13	111	9.9	252	2 B88637	protein W09G12.4 [
14	86	7.7	826	2 A60385	monocyte surface a
15	85.5	7.7	727	2 JC7818	metalloproteinase
16	85	7.6	281	2 D88637	protein W09G12.1 [
17	85	7.6	814	2 G02390	disintegrin-like m
18	85	7.6	2318	2 S45306	notch 3 protein -
19	84	7.5	334	2 T23027	hypothetical prote
20	83.5	7.5	543	2 T20964	hypothetical prote
21	83.5	7.5	1574	2 T13954	MEGF6 protein - R
22	83	7.4	660	2 S31437	homeotic protein - h
23	82	7.3	2531	2 S18188	notch protein homo
24	82	7.3	2531	2 A46019	notch-1 protein -
25	81.5	7.3	345	2 T16074	hypothetical prote
26	81.5	7.3	4135	2 T14229	tenascin-X - bovin
27	81	7.3	2406	2 A54148	odz protein - frul
28	81	7.3	2515	2 S47008	tenascin-like prot
29	81	7.3	4545	1 S25111	alpha-2-macroglobu

30 80.5 7.2 2403 2 A59386 sanko - human
31 80 7.2 647 2 A43902 tenascin - eastern
32 80 7.2 662 2 I37892 IL12 receptor comp
33 79.5 7.1 877 2 T43449 hypothetical prote
34 79.5 7.1 1045 2 A29840 serine proteinase
35 79 7.1 724 2 B82186 catalase/peroxidase
36 79 7.1 1639 1 MMFFB2 laminin gamma-1 ch
37 79 7.1 2321 2 S78549 notch3 protein - h
38 78.5 7.0 378 2 B59180 Wnt inhibitory fac
39 78.5 7.0 476 1 SGMSV vitronectin precur
40 78.5 7.0 2703 1 A24420 notch protein - fr
41 78.5 7.0 3006 2 T28625 variant-specific s
42 78 7.0 423 2 T14531 S-locus-specific g
43 78 7.0 1364 2 T00250 MEGF2 protein - hu
44 78 7.0 1984 2 T13171 probable vitelloge
45 78 7.0 2195 2 T34264 hypothetical prote

ALIGNMENTS

RESULT 1

A56136

jagged protein precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 11-Jan-2000

C:Accession: A56136

R:Lindseil, C.E.; Shawber, C.J.; Boulter, J.; Weinmaster, G.

Cell 80, 909-917, 1995

A:Title: Jagged: a mammalian ligand that activates Notch1.

A:Reference number: A56136; MUID:95211842; PMID:7697721

A:Accession: A56136

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1220 <LIN>

A:Cross-references: GB:L38483

C:Superfamily: unassigned EGF-related proteins; EGF homology

F:379-410/Domain: EGF homology <EGF1>

F:492-523/Domain: EGF homology <EGF>

F:634-665/Domain: EGF homology <EGF2>

Query Match 93.6%; Score 1044.5; DB 2; Length 1220;
Best Local Similarity 93.1%; Pred. No. 5.8e-86;
Matches 188; Conservative 3; Mismatches 4; Indels 7; Gaps 2;

QY	1	SGQFELEILSMQNVNGELQNGCCGGARNFG----	DRKCTFDECDTFKVKCLKKEYQSRVT	56
DB	32	SGQFELEILSMQNVNGELQNGCCA----	EPGLVPRPKCTRDECDTFKVKCLKKEYQSRVT	88
QY	57	AGGPCSPGSGSTPVIGGNTNLKASRGNDNRNRLVLP	PSFAWPRSYTLVLEAWDSSNDTVQ	116
DB	89	AGGPCSPGSGSTPVIGGNTNLKASRGNDNRNRLVLP	PSFAWPRSYTLVLEAWDSSNDTIQ	148
QY	117	PDSIIKASHGMINPSROMOTLKQNTVAHFEYQIRVTC	DDYVYGGCNKFCRPRDDFF	176
DB	149	PDSIIKASHGMINPSROMOTLKQNTVAHFEYQIRVTC	DDYVYGGCNKFCRPRDDFF	208
QY	177	GHVACDQNGNKTCMEGWMGPEC	198	
DB	209	GHVACDQNGNKTCMEGWMGPEC	230	

RESULT 2

S16148

gene serrate protein precursor - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 31-Dec-1991 #sequence_revision 02-Aug-1994 #text_change 17-Nov-2000

C:Accession: S16148; S16878; A36666

R:Thomas, U.; Speicher, S.A.; Knust, E.

Development 111, 749-761, 1991

A:Title: The Drosophila gene Serrate encodes an EGF-like transmembrane protein with a

A:Reference number: S16148; MUID:91347903; PMID:1840519

A:Accession: S16148

A:Molecule type: mRNA
A:Residues: 1-1408 <THO1>
A:Cross-references: EMBL:X56811
R:Thomas, U.
Submitted to the EMBL Data Library, November 1990
A:Reference number: S16878
A:Accession: S16878
A:Molecule type: mRNA
A:Residues: 1-1351, T', 1353-1408 <THO2>
A:Cross-references: EMBL:X56811; NID:g8563; PID:g8564
R:Fleming, R.J.; Scottgale, T.N.; Diederich, R.J.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2188-2201, 1990
A:Title: The gene *Serrate* encodes a putative EGF-like transmembrane protein essential for
A:Reference number: A36666; MUID:91099666; PMID:2125287
A:Accession: A36666
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15, 20-26, A', 28-1408 <FLE>
A:Cross-references: GB:M35759; NID:g158605; PID:g158606
C:Genetics:
A:Gene: FlyBase:Ser
A:Cross-references: FlyBase:FBgn0004197
C:Superfamily: unassigned EGF-related proteins; EGF homology
C:Keywords: glycoprotein; transmembrane protein
F:1-84/Domain: signal sequence #status predicted <SIG>
F:85-1408/Domain: gene serrate protein #status predicted <MAT>
F:85-1221/Domain: extracellular #status predicted <EXT>
F:283-316/Domain: EGF homology <EG01>
F:319-348/Domain: EGF homology <EG02>
F:355-388/Domain: EGF homology <EG03>
F:395-488/Domain: EGF homology #status
F:495-526/Domain: EGF homology <EG05>
F:533-608/Domain: EGF homology #status atypical <EG04>
F:615-645/Domain: EGF homology #status atypical <EG06>
F:652-683/Domain: EGF homology <EG07>
F:690-720/Domain: EGF homology <EG08>
F:727-796/Domain: EGF homology #status atypical <EG10>
F:803-834/Domain: EGF homology <EG11>
F:841-876/Domain: EGF homology <EG12>
F:883-914/Domain: EGF homology <EG13>
F:921-952/Domain: EGF homology <EG14>
F:997-1060/Region: cysteine-rich
F:1222-1246/Domain: transmembrane #status predicted <TM1>
F:1247-1408/Domain: intracellular #status predicted <INT>
F:152,196,247,331,412,452,558,739,965,977,1004,1030,1150/Binding site: carbohydrate (Asn
Query Match 40.0%; Score 446; DB 2; Length 1408;
Best Local Similarity 43.5%; Pred. No. 5.7e-32;
Matches 91; Conservative 32; Mismatches 66; Indels 20; Gaps 7;
P: 1 SGOFELILSMQNVNGLONGNCCGAGRNPGDRKCTR---DECDYFKVCLKEYQ--- 52
D: 84 AGNFELEILSNTNSHLNGVCCG---MPAELRATKTCGSPCTAFRLCLKEYQTTEQ 140
Q: 53 -SRVTAGGCGSGSTPVIGGNTFNLKASGRNRRIVLPFSFAWPRSYTLLEAVDSS 111
D: 141 GASISTG--CSFGNATTKILGSSSVLS--DPGVGAIVLPFTFRWTKSFTLILQALDYM 195
Q: 112 NTVQPDSS--IIEKASHSGMINPSRQWQTLKONTGVAHFEYQIRVTCDDYYGFGCNKFC 169
D: 196 N-TSPDAERLLEETSYSGVILPSPPEWTKLDIRGNARITYRVVQCAVITYNTTCTTFC 254
Q: 170 RPRDDFFGHYACDQNGKNTCMGWMGPEC 198
D: 255 RPRDDQFGHYACGSEGGKCLNGWGVNC 283
RESULT 3
I50719
C:Delta-1 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02-Aug-2002
C:Accession: I50719

R:Henrique, D.; Adam, J.; Myat, A.; Chitnis, A.; Lewis, J.; Ish-Horowicz, D.
Nature 375, 787-790, 1995
A:Title: Expression of a Delta homologue in prospective neurons in the chick.
A:Reference number: I50719; MUID:95319507; PMID:7596411
A:Accession: I50719
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-728 <HEN>
A:Cross-references: EMBL:U26590; NID:g882411; PIDN:AAC59689.1; PID:g882412
C:Superfamily: delta-4 protein; EGF homology
F:299-332/Domain: EGF homology <EGX1>
F:339-370/Domain: EGF homology <EGF1>
F:416-447/Domain: EGF homology <EGX2>
F:454-485/Domain: EGF homology <EGF>
F:492-523/Domain: EGF homology <EGF3>
Query Match 38.8%; Score 433.5; DB 2; Length 728;
Best Local Similarity 39.4%; Pred. No. 3.6e-31;
Matches 82; Conservative 35; Mismatches 78; Indels 13; Gaps 5;
Q: 1 SGOFELILSMQNVNGLONGNCC--GGARNPCDRKCTRDECDYFKVCLKEYQSRVTAG 58
D: 24 SGVFEKLQFEVFNKKGLLSNRCCGGGPGGAGQQC---DCKTFRVCLKHQASVSPE 80
Q: 59. GPCSGSGSTPVIGGNTFNLKASRGND---RRNIVLPFSFAWPRSYTLLEVA--WDSSN 112
D: 81 PCTYGSATPVLGANSFVDPGAGADPAFNSPIRPFPGFTWPGFSLIEALHTDSDP 140
Q: 113 D--TVOPDSIIIEKASHSGMINPSRQWQTLKONTGVAHFEYQIRVTCDDYYGFGCNKFC 170
D: 141 DLTTPENRILSLRATQRHLAVGEWSQDLHSSGRDILKYSYRFVCDHYGEGCSVFGR 200
Q: 171 PRDDFFGHYACDQNGKNTCMGWMGPEC 198
D: 201 PRDDRFGHFTCGERGEKVCNPGWKQGYC 228
RESULT 4
S19087
gene Delta protein precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Aug-2002
C:Accession: S19087
R:Muskavitch, M.A.T.
Submitted to the EMBL Data Library, June 1991
A:Reference number: S19087
A:Accession: S19087
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-833 <MUS>
A:Cross-references: EMBL:Y00222
C:Genetics:
A:Gene: FlyBase:Dl
A:Cross-references: FlyBase:FBgn0000463
C:Superfamily: neurogenic protein delta; EGF homology
F:335-371/Domain: EGF homology <EGF1>
F:378-415/Domain: EGF homology <EGX1>
F:457-488/Domain: EGF homology <EGF>
F:533-564/Domain: EGF homology <EGF3>
Query Match 37.9%; Score 423; DB 2; Length 833;
Best Local Similarity 39.5%; Pred. No. 3.7e-30;
Matches 81; Conservative 32; Mismatches 84; Indels 8; Gaps 4;
Q: 1 SGOFELILSMQNVNGLONGNCCGAGRNPGDRKCTRDECDYFKVCLKEYQSRVTAGP 60
D: 23 SGSEFLRLKYFSDHGRDNEGRCCSGESDGATGKCL-GSCKTRFRVCLKHQATIDTTSQ 81
Q: 61 CSFGSGSTPVIGGNTFNL-KASRGND---NRIVLPFSFAWPRSYTLLEAVDSSNDTVQ 116
D: 82 CYGVGVTPILGNSVNLTDQRFONKGTNPQLQFSPFSWPGFTSLIVAEVHDTNNSN 141
Q: 117 PDS---IIEKASHSGMINPSRQWQTLKONTGVAHFEYQIRVTCDDYYGFGCNKFCRPRD 173

Db 142 ARTNKLIIQLRLVVOVLEVSSEWTKNSQSYTSLFYDFRVTCDLNLYGSCAKFCRPRD 201

Qy 174 DFFGHYACDQNGNKTCEGWMGPEC 198

Db 202 DSFGHSTCSETGEIICLTGMOGDYC 226

RESULT 5

A31246 neurogenic protein Delta precursor - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 02-Aug-2002

C:Accession: A31246

R:Kopczynski, C.C.; Alton, A.K.; Fechtel, K.; Kooh, P.J.; Muskavitch, M.A.T.

Genes Dev. 2, 1723-1735, 1988

A:Title: Delta, a Drosophila neurogenic gene, is transcriptionally complex and encodes a

A:Reference number: A31246; MUID:89196890; PMID:3149249

A:Accession: A31246

A:Molecule type: mRNA

A:Residues: 1-832 <KOP>

A:Cross-references: GB:Y00222

C:Genetics:

A:Gene: FlyBase:D1

A:Cross-references: FlyBase:FBgn0000463

C:Superfamily: neurogenic protein delta; EGF homology

F:295-328/Domain: EGF homology <EGX1>

F:422-450/Domain: EGF homology <EGF1>

F:457-488/Domain: EGF homology <EGF>

F:533-564/Domain: EGF homology <EGF3>

Query Match 37.6%; Score 420; DB 2; Length 832;

Best Local Similarity 39.0%; Pred. No. 6.9e-30;

Matches 80; Conservative 33; Mismatches 84; Indels 8; Gaps 4;

Qy 1 SGQFELEILSMQNVNGELQNGCCGARNPGDRKTRDECDTYFKVCLKEYQSRVTAGGP 60

Db 23 SGSEFLRLKYFSNDHGRDNEGRCCSGESDGTGKCL-GSCKTRFLCLKHQATIDTTSQ 81

Qy 61 CSFGSGSTPVIGGNTFNL-KASRGNDR---NRIVLPFSFAWPRSYTLLEVAWDSNDTVQ 116

Db 82 CTYGDVITPILGENSVNLTDQRFQNGFTNPIQPFESFSPGTFSLIVEAWHDTNNSGN 141

Qy 117 PDS---IIEKASHSGMINPSROWOTLKONTGVAHFYQIRVTCDDYYGFCGNKFCRPRD 173

Db 142 ARTNKLIIQLRLVVOVLEVSSEWTKNSQSYTSLFYDFRVTCDLNLYGSCAKFCRPRD 201

Qy 174 DFFGHYACDQNGNKTCEGWMGPEC 198

Db 202 DSFGHSTCSETGEIICLTGMOGDYC 226

RESULT 6

S00670

neurogenic repetitive locus delta protein precursor - fruit fly (Drosophila melanogaster)

N:Alternate names: gene D1 protein

C:Species: Drosophila melanogaster

C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 02-Aug-2002

C:Accession: S00670; A26637

R:Vaessin, H.; Bremer, K.A.; Knust, E.; Campos-Ortega, J.A.

EMBO J. 6, 3431-3440, 1987

A:Title: The neurogenic gene Delta of Drosophila melanogaster is expressed in neurogenic

A:Accession: S00670

A:Molecule type: mRNA

A:Residues: 1-880 <VAE>

A:Cross-references: EMBL:X06289; NID:g7853

R:Knust, E.; Dietrich, U.; Tepass, U.; Bremer, K.A.; Weigel, D.; Vaessin, H.; Campos-Ortega

EMBO J. 6, 761-766, 1987

A:Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and

A:Reference number: A91081; MUID:87218537; PMID:3107986

A:Accession: A26637

A:Molecule type: mRNA

A:Residues: 422-436, 'ET', 439-458, 'A', 460-489, 'T', 491-621 <KND>
A:Cross-references: GB:X05140; NID:g7851; PIDN:CAA28786.1; PID:g929563

C:Genetics:

A:Gene: Delta; D1

A:Cross-references: FlyBase:FBgn0000463

C:Superfamily: neurogenic protein delta; EGF homology

C:Keywords: transmembrane protein

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-88/product: neurogenic repetitive locus delta protein #status predicted <MAT>

F:457-488/Domain: EGF homology <EGF1>

F:533-564/Domain: EGF homology <EGF2>

Query Match 37.6%; Score 420; DB 2; Length 880;

Best Local Similarity 39.0%; Pred. No. 7.4e-30;

Matches 80; Conservative 33; Mismatches 84; Indels 8; Gaps 4;

Qy 1 SGQFELEILSMQNVNGELQNGCCGARNPGDRKTRDECDTYFKVCLKEYQSRVTAGGP 60

Db 23 SGSEFLRLKYFSNDHGRDNEGRCCSGESDGTGKCL-GSCKTRFLCLKHQATIDTTSQ 81

Qy 61 CSFGSGSTPVIGGNTFNL-KASRGNDR---NRIVLPFSFAWPRSYTLLEVAWDSNDTVQ 116

Db 82 CTYGDVITPILGENSVNLTDQRFQNGFTNPIQPFESFSPGTFSLIVEAWHDTNNSGN 141

Qy 117 PDS---IIEKASHSGMINPSROWOTLKONTGVAHFYQIRVTCDDYYGFCGNKFCRPRD 173

Db 142 ARTNKLIIQLRLVVOVLEVSSEWTKNSQSYTSLFYDFRVTCDLNLYGSCAKFCRPRD 201

Qy 174 DFFGHYACDQNGNKTCEGWMGPEC 198

Db 202 DSFGHSTCSETGEIICLTGMOGDYC 226

RESULT 7

JC7570

Delta-4 protein - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 16-Aug-2002

C:Accession: JC7570

R:Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Miyatani, S.

J. Biochem. 129, 27-34, 2001

A:Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.

A:Reference number: JC7569; MUID: 21064937; PMID:11134954

A:Accession: JC7570

A:Molecule type: mRNA

A:Residues: 1-685 <YON>

A:Cross-references: DDBJ:AB043894

C:Comment: This protein, a member of the Notch family of proteins, is a transmembrane
ates the Notch signaling, the growth or differentiation of vascular endothelial cells

C:Genetics:

A:Gene: delta-4

C:Superfamily: delta-4 protein; EGF homology

C:Keywords: transmembrane protein

Query Match 37.6%; Score 419.5; DB 2; Length 685;

Best Local Similarity 38.2%; Pred. No. 6.2e-30;

Matches 78; Conservative 40; Mismatches 67; Indels 19; Gaps 5;

Qy 1 SGQFELEILSMQNVNGELQNGCCGARNPGDRKTRDECDTYFKVCLKEYQSRVTAGGP 60

Db 27 SGVFQLQLQEFINERGVLASGRPC-----EPG-----CRTFFRVCLKHQA-VVSPGP 73

Qy 61 CSFGSGSTPVIGGNTFNL-KASRGNDRNRIVLPFSFAWPRSYTLLEVAWDSNDTVQ--- 116

Db 74 CTGTGTVPVLGTNTSFAVRDSSGGGRNPLQLPFTWPGTFSLIIIEAWHAGDGLRPEA 133

Qy 117 --PDSIIIEKASHSGMINPSROWOTLKONTGVAHFYQIRVTCDDYYGFCGNKFCRPRD 174

Db 134 LPPDALLSKIAIQSLAVGQNWLLDEQTSITLRLRYSYRVICSDNYNYGDCNCSLCKKRRND 193

Qy 175 FFGHYACDQNGNKTCEGWMGPEC 198

Db 194 HFGHYVCPDGNLSCLPCWTGEYC 217

```

RESULT 8
I48324
DELTA-like 1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Aug-2002
C:Accession: I48324
R: Bettenhausen, B.; de Angelis, M.H.; Simon, D.; Guenet, J.L.; Gossler, A.
Development 121, 2407-2418, 1995
A:Title: Transient and restricted expression during mouse embryogenesis of Dll1, a murin
A:Reference number: I48324; MUID:95401858; PMID:7671806
A:Accession: I48324
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-722 <RES>
A:Cross-references: EMBL:X80903; NID:9806569; PIDN:CAA56865.1; PID:9806570
C:Genetics:
A:Gene: Dll1
C:Superfamily: delta-4 protein; EGF homology
F:331-362/Domain: EGF homology <EGF2>
F:446-477/Domain: EGF homology <EGF>
F:484-515/Domain: EGF homology <EGF1>

Query Match 37.6%; Score 419.5; DB 2; Length 722;
Best Local Similarity 40.0%; Pred. No. 6.6e-30;
Matches 82; Conservative 30; Mismatches 80; Indels 13; Gaps 5;

QY 1 SQGFELILSMONVNGELONGCCGARNPGDRKTRDECDYFKVCLKEYQSRVTAGGP 60
Db 22 SGVFLKLQEFVYKGLGNCRGSGP---PCA---CRTFFRVCLKHQASVSEPP 75

QY 61 CSFGSGSTPVIGNTFNKASRGND---RNRIVLPFSFAMPRSYTLLEA--WDSND-- 113
Db 76 CYGSAVTPVLGVDSFLPDGAGIDPAFSNPRFFEGFTWPGTFSLIIEALHTDSDDLA 135

QY 114 TVOPDSITEKASHGMINPSROWQTLKONTGVAHFEYQIRVTCDDYVYGFGCNFKCRPRD 173
Db 136 TENPERLISRLTORHLTVGEESQDLHSSGRTDLRYSYRFVCDHEHYEGGCVFRCPRD 195

QY 174 DFEHGYACDQNGKTCMEGWMGPEC 198
Db 196 DAFGHFTCGDRGKMDPGWKGQYC 220

RESULT 9
JC7569
Delta-4 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 16-Aug-2002
C:Accession: JC7569
R: Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.;
J. Biochem. 129, 27-34, 2001
A:Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.
A:Reference number: JC7569; MUID: 21064937; PMID:11134954
A:Accession: JC7569
A:Molecule type: mRNA
A:Residues: 1-686 <VON>
A:Cross-references: DDBJ:AB043893
C:Comment: This protein, a member of the Notch family of proteins, is a transmembrane re
aces the Notch signaling, the growth or differentiation of vascular endothelial cells.
C:Genetics:
A:Gene: delta-4
C:Superfamily: delta-4 protein; EGF homology

Query Match 36.8%; Score 410.5; DB 2; Length 686;
Best Local Similarity 37.3%; Pred. No. 4e-29;
Matches 76; Conservative 41; Mismatches 68; Indels 19; Gaps 5;

QY 1 SQGFELILSMONVNGELONGCCGARNPGDRKTRDECDYFKVCLKEYQSRVTAGGP 60
Db 28 SGIFQLRLQEFVNRQGMLANGOSC-----EPG-----CRTFFRICLKHFOATFSE-GP 74
```

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QY 61 CSFGSGSTPVIGNTFNKASRGNDNRNIVLPFSFAMPRSYTLLEA--WDSNDYVQPD- 118
Db 75 CTFGNVSTPVLGTSNPFVRDKNKSGRNPQLQFPENFTWPTCTFSLNIQAWHTPCDDLRPET 134

QY 119 ----STIEKASHGMINPSROWQTLKONTGVAHFEYQIRVTCDDYVYGFGCNFKCRPRD 174
Db 135 SPGNSLSIIQIIQGSIAVGKIWRDQNDTLRLSYSYRVICSDNYGSCSLCKRKDD 194

QY 175 FGHYACDQNGKTCMEGWMGPEC 198
Db 195 HFGHYEQPDGSLSLCLPGWTGKYC 218

RESULT 10
T16213
APX-1 protein homolog - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C:Accession: T16213
R: Bentley, D.
submitted to the EMBL Data Library, May 1996
A:Description: the sequence of C. elegans cosmid F31A9.
A:Reference number: Z18479
A:Accession: T16213
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-379 <BEN>
A:Cross-references: EMBL:U58738; NID:g1326302; PID:g1326305; PIDN:AAB00603.1; GSPDB:G
A:Experimental source: strain Bristol N2; clone F31A9
C:Genetics:
A:Gene: CBSP:arg-1
A:Map position: X
A:Introns: 92/1; 133/2; 174/1; 225/1; 307/1; 342/3

Query Match 11.2%; Score 125.5; DB 2; Length 379;
Best Local Similarity 23.6%; Pred. No. 0.00098;
Matches 49; Conservative 18; Mismatches 74; Indels 67; Gaps 8;

QY 1 SQGFELILSMONVNGELONGCCGARNPGDRKTRDECDYFKVCLKEYQSRVTAGGP 60
Db 21 SGIIELLISPOSV---LIKSTACAFKCP-----VHDELSVPRNV----- 58

QY 61 CSFGSGSTPVIGNTFNKASRGNDNRNIVLPFSFAMPRSYTLLEA--WDSNDYVQPD 119
Db 59 ----EGGVPL---RTHIGYRGEARQNLDFEILPEPSTNEMIALEQHRAPSDT----- 105

QY 120 IIEKASHGMINPSROWQTLKONTGVA-----HFEYQIRVTCDDYVYGFGCNFKCR 170
Db 106 -----KWTGLPIVIETTLGFNTVHLRNVCTSNYYGKRCNRYCI 145

QY 171 PRDDFFGHYACDQNGKTCMEGWMGPEC 198
Db 146 PSPAL--HWCSTNGVRQCAVWGWDCC 171

RESULT 11
D88991
protein apx-1 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: D88991
R: anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C-
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A:Accession: D88991
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-513 <STO>
A:Cross-references: GB:chr_V; PIDN:AAC69353.1; PID:g3808343; GSPDB:GN00023
C:Genetics:
```

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/

C: Date: 03-Jun-2002 #sequence:

1

c, species: *Arceomionas* sp. (strain 077)
c: Date: 03-Jun-2002 #sequence revision 03-Jun-2002 #text change 03-Jun-2002

C;Accession: JC7818
R;Miyamoto, K.; Tsujibo, H.; Nukui, E.; Itoh, H.; Kaidzu, Y.; Inamori, Y.
Biosci. Biotechnol. Biochem. 66, 416-421, 2002
A;Title: Isolation and characterization of the genes encoding two metalloproteases (MprI
A;Reference number: JC7818; PMID:11999419; MUID:21994062
A;Accession: JC7818
A;Molecule type: DNA
A;Residues: 1-727 <MIY>
A;Cross-references: DDBJ:AB063611
A;Experimental source: strain O-7
C;Comment: This enzyme, an extracellular alkaline metalloprotease, showing high similarity
C;Genetics:
A;Gene: mprI
A;Start codon: GTG

Query Match 7.7%; Score 85.5; DB 2; Length 727;
Best Local Similarity 22.9%; Pred. No. 8.2;
Matches 52; Conservative 24; Mismatches 82; Indels 69; Gaps 13;
QY 9 LSMQNVNGELQNGNCCGGARNP-----GDRKCTRDECDTYFKVCLKEYQ----- 52
Db 494 LAAGVNSNLSTGSSCD--TNPPPPGDEELTNGQPTGISCAAKEQMEFFTLDVPADAT 551
QY 53 --SRVTAGGPCSFGS-----GSTPVIGGNTFNKASRGNDNRNRIVLPPSFAWPRSXYTL 103
Db 552 SLNFTTSGGS---GDADLYVKYGSRPRLNTYDCNSTTSTSNESCDI-----SNIQAGKYV 604
QY 104 LVEAWD-----SSNDIVQPDIIIEKASHSGMINPSROWQTLKQNTGVAHEFYQI 152
Db 605 MVEAWNQISGVTLTGYSSTGTQP---IDR-TESNVSVASGSWTRFTQDLNASYSSLEV 660
QY 153 RVTCD----DYXYGFCNKF-----CRPRDFFGHYACDQNG-NKTC 189
Db 661 SISGSGDADLYVNFSGSTTSYQCRP-----FKNGNNEIC 697

Search completed: August 25, 2003, 17:55:29
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2003, 17:43:38 ; Search time 23 Seconds
(without alignments)
404.839.Million cell updates/sec

Title: US-09-995-593A-5
Perfect score: 1116
Sequence: 1 SQGFELLSMQNVGELQN.....YACDQNGKTCMEGWMGPEC 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1116	100.0	1218	1 JAG1_HUMAN	P78504 rat mus sapien
2	1109	99.4	1219	1 JAG1_HUMAN	Q63722 rattus norv
3	1102	98.7	1218	1 JAG1_MOUSE	Q9qxx0 mus musculu
4	849	76.1	1213	1 JAG3_BRARE	Q90y54 brachydanio
5	830	74.4	1242	1 JAG1_BRARE	Q90y57 brachydanio
6	659	59.1	1247	1 JAG2_MOUSE	Q9qy65 mus musculu
7	652	58.4	1238	1 JAG2_HUMAN	Q9y219 homo sapien
8	597	53.5	1202	1 JAG2_RAT	P97607 rattus norv
9	446	40.0	1408	1 SERR_DROME	P18168 drosophila
10	431	38.6	723	1 DLL1_HUMAN	O00548 homo sapien
11	423	37.9	833	1 DLL_DROME	P10041 drosophila
12	419.5	37.6	685	1 DLL4_HUMAN	Q9nr61 homo sapien
13	419.5	37.6	722	1 DLL1_MOUSE	Q61483 mus musculu
14	413.5	37.1	714	1 DLL1_RAT	P97677 rattus norv
15	410.5	36.8	686	1 DLL4_MOUSE	Q9j171 mus musculu
16	192	17.2	618	1 DLL3_HUMAN	Q9ny17 homo sapien
17	170	15.2	592	1 DLL3_MOUSE	Q88516 mus musculu
18	169	15.1	589	1 DLL3_RAT	Q88671 rattus norv
19	118.5	10.6	515	1 APX1_CAEEL	P41990 caenorhabdi
20	114	10.2	402	1 LAG2_CAEEL	P45442 caenorhabdi
21	100	9.0	815	1 AD15_MOUSE	Q88839 mus musculu
22	96.5	8.6	956	1 AD19_HUMAN	Q9h013 homo sapien
23	96	8.6	920	1 AD19_MOUSE	Q35674 mus musculu
24	95	8.5	816	1 AD15_RAT	Q9qyv0 r adam 15 p
25	89	8.0	3312	1 CLR3_HUMAN	Q9nyq7 homo sapien
26	87.5	7.8	776	1 AD28_MACFA	Q9xsl6 macaca fasc
27	86	7.7	826	1 AD08_MOUSE	Q05910 mus musculu
28	85	7.6	814	1 AD15_HUMAN	Q13444 homo sapien
29	85	7.6	2318	1 NTC3_MOUSE	Q61982 mus musculu
30	85	7.6	2319	1 NTC3_RAT	Q9r172 rattus norv
31	82.5	7.4	661	1 HT31_ARATH	Q04996 arabidopsis
32	82	7.3	2531	1 NTC1_MOUSE	Q01705 mus musculu
33	82	7.3	2531	1 NTC1_RAT	Q07008 rattus norv

RESULT 1

ID	JAG1_HUMAN	STANDARD	PRT	1218 AA
AC	P78504	O14902; O15122; Q15816;		
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DE	Jagged 1 precursor (Jagged1) (hvl).			
GN	JAG1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97422615; PubMed=9268641;			
RA	Oda T., Elkhoulou A.G., Meltzer P.S., Chandrasekharappa S.C.;			
RT	"Identification and cloning of the human homolog (JAG1) of the rat			
RT	Jagged1 gene from the Alagille syndrome critical region at 20p12.;			
RL	Genomics 43:376-379(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND VARIANT AGS CYS-184.			
RC	TISSUE=Bone marrow;			
RX	MEDLINE=97351506; PubMed=9207788;			
RA	Li L., Krantz I.D., Deng Y., Genin A., Banta A.B., Collins C.C.;			
RA	Qi M., Trask B.J., Kuo W.L., Cochran J., Costa T., Pierpont M.E.M.;			
RA	Rand E.B., Piccoli D.A., Hood L., Spinner N.B.;			
RT	"Alagille syndrome is caused by mutations in human Jagged1, which			
RT	encodes a ligand for Notch1.;"			
RL	Nat. Genet. 16:243-251(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND FUNCTION.			
RX	MEDLINE=98122342; PubMed=9462510;			
RA	Li L., Milner L.A., Deng Y., Iwata M., Banta A.B., Graf L.;			
RA	Marcovina S., Friedman C., Trask B.J., Hood L., Torok-Storb B.;			
RT	"The human homolog of rat Jagged1 expressed by marrow stroma inhibits			
RT	differentiation of 32D cells through interaction with Notch1.;"			
RL	Immunity 8:43-55(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Cervical carcinoma;			
RX	MEDLINE=99262417; PubMed=10329626;			
RA	Bash J., Zong W.-X., Banga S., Rivera A., Ballard D.W., Ron Y.;			
RA	Gelinas C.;			
RT	"Rel/NF-kappaB can trigger the Notch signaling pathway by inducing the			
RT	expression of Jagged1, a ligand for Notch receptors.;"			
RL	EMBO J. 18:2803-2811(1999).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99180765; PubMed=10079256;			
RA	Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L., S.;			
RA	Banks A., Teiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;			
RT	"Human ligands of the Notch receptor.;"			
RL	Am. J. Pathol. 154:785-794(1999).			
RN	[6]			
RP	SEQUENCE FROM N.A.			

Q9wu60 mus musculu
P33792 escherichia
Q99466 homo sapien
P42701 homo sapien
Q9ukq2 homo sapien
P09489 serratia ma
Q9jln6 mus musculu
P15215 drosophila
Q9um47 homo sapien
P46531 homo sapien
P58751 rattus norv
Q9w6f9 brachydanio

ALIGNMENTS

RX MEDLINE-21638749; PubMed-11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Babbage A.K., Baggeley C.L.,
 RA Jones M., Stavridis G., Almeida J.P., Babbage A.K., Baggeley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grahame D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Levaeslaitho M.A.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN [7]
 RP SEQUENCE OF 14-1227 FROM N.A.
 RC TISSUE-Umbilical vein endothelial cells;
 RX MEDLINE-97115768; PubMed-8955070;
 RA Zimin A.B., Pepper M.S., McMahon G.A., Nguyen F., Montesano R.,
 RA Maciag T.;
 RT "An antisense oligonucleotide to the notch ligand jagged enhances
 RT fibroblast growth factor-induced angiogenesis in vitro.";
 RL J. Biol. Chem. 271:32499-32502(1996).
 RN [8]
 RP DISPEASE.
 RX MEDLINE-97351505; PubMed-9207787;
 RA Oda T., Elkahoul A.G., Pike B.L., Okajima K., Krantz I.D., Genin A.,
 RA Piccoli D.A., Meltzer P.S., Spinner N.B., Collins F.S.,
 RA Chandrasekharappa S.C.;
 RT "Mutations in the human Jagged1 gene are responsible for Alagille
 RT syndrome.";
 RL Nat. Genet. 16:235-242(1997).
 RN [9]
 RP DEVELOPMENTAL STAGE.
 RX MEDLINE-20436345; PubMed-10979356;
 RA Jones E.A., Clement-Jones M., Wilson D.I.;
 RT "Jagged1 expression in human embryos: correlation with the Alagille
 RT syndrome phenotype.";
 RL J. Med. Genet. 37:663-668(2000).
 RN [10]
 RP VARIANTS AGS CYS-184 AND HIS-184.
 RX MEDLINE-98254456; PubMed-9585603;
 RA Krantz I.D., Colliton R.P., Genin A., Rand E.B., Li L., Piccoli D.A.,
 RA Spinner N.B.;
 RT "Spectrum and frequency of jagged1 (JAG1) mutations in Alagille
 RT syndrome patients and their families.";
 RL Am. J. Hum. Genet. 62:1361-1369(1998).
 RN [11]
 RP VARIANTS AGS HIS-79; THR-127; ARG-129; LEU-163; GLY-184; SER-187;
 RP GLX-229; PHE-288; CYS-288; PHE-438; SER-731 AND ARG-740.
 RX MEDLINE-98236888; PubMed-10220506;
 RA Crosnier C., Driancourt C., Raynaud N., Dhorne-Pollet S., Pollet N.,
 RA Bernard O., Hadchouel M., Meunier-Rotival M.;
 RT "Mutations in JAGGED1 gene are predominantly sporadic in Alagille
 RT syndrome.";
 RL Gastroenterology 116:1141-1148(1999).
 RN [12]
 RP VARIANTS AGS THR-152 AND LEU-184.
 RX MEDLINE-20004539; PubMed-10533065;

RA Pilia G., Uda M., Macis D., Frau F., Crisponi L., Balli F.,
 RA Barbera C., Colombo C., Frediani T., Gatti R., Iorio R., Marazzi M.G.,
 RA Marcellini M., Musumeci S., Nebbia G., Vajro P., Ruffa G., Zancan L.,
 RA Cao A., Devirgillis S.;
 RT "Jagged-1 mutation analysis in Italian Alagille syndrome patients.";
 RL Hum. Mutat. 14:394-400(1999).
 RN [13]
 RP VARIANTS AGS TYR-229 AND ARG-386.
 RX MEDLINE-20514559; PubMed-11058898;
 RA Heritage M.L., Macmillan J.C., Colliton R.P., Genin A., Spinner N.B.,
 RA Anderson G.J.;
 RT "Jagged1 (JAG1) mutation detection in an Australian Alagille syndrome
 RT population.";
 RL Hum. Mutat. 16:408-416(2000).
 RN [14]
 RP VARIANT TOF ASP-274.
 RX MEDLINE-21067871; PubMed-11152664;
 RA Elgadah Z.A., Hamosh A., Biery N.J., Montgomery R.A., Duke M.,
 RA Elkins R., Dietz H.C.;
 RT "Familial Tetralogy of Fallot caused by mutation in the jagged1
 RT gene.";
 RL Hum. Mol. Genet. 10:163-169(2001).
 RN [15]
 RP VARIANT AGS SER-37.
 RX MEDLINE-21096916; PubMed-11157803;
 RA Morrisette J.D., Colliton R.P., Spinner N.B.;
 RT "Defective intracellular transport and processing of JAG1 missense
 RT mutations in Alagille syndrome.";
 RL Hum. Mol. Genet. 10:405-413(2001).
 RN [16]
 RP VARIANTS AGS PHE-220 AND ARG-753.
 RX MEDLINE-20579880; PubMed-11139247;
 RA Crosnier C., Driancourt C., Raynaud N., Hadchouel M.,
 RA Meunier-Rotival M.;
 RT "Fifteen novel mutations in the JAGGED1 gene of patients with Alagille
 RT syndrome.";
 RL Hum. Mutat. 17:72-73(2001).
 CC -!- FUNCTION: Ligand for multiple Notch receptors and involved in the
 CC mediation of Notch signaling. May be involved in cell-fate
 CC decisions during hematopoiesis. Seems to be involved in early
 CC and late stages of mammalian cardiovascular development. Inhibits
 CC myoblast differentiation (by similarity). Enhances fibroblast
 CC growth factor-induced angiogenesis (in vitro).
 CC -!- SUBUNIT: Interacts with NOTCH1, NOTCH2 AND NOTCH3 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues.
 CC In cervix epithelium expressed in undifferentiated subcolumnar
 CC reserve cells and squamous metaplasia. Expression is up-regulated
 CC in cervical squamous cell carcinoma. Expressed in bone marrow cell
 CC line HS-27a which supports the long-term maintenance of immature
 CC progenitor cells.
 CC -!- DEVELOPMENTAL STAGE: Expressed in 32-52 days embryos in the distal
 CC cardiac outflow tract and pulmonary artery, major arteries, portal
 CC vein, optic vesicle, otocyst, branchial arches, metanephros,
 CC pancreas, mesocardium, around the major bronchial branches, and in
 CC the neural tube.
 CC -!- DISEASE: Defects in JAG1 are the cause of Alagille syndrome (AGS),
 CC an autosomal dominant developmental disorder that affects structures
 CC in the liver, heart, skeleton, eye, kidney, and other organs.
 CC -!- DISEASE: Defects in JAG1 are associated with right heart
 CC obstructive disease variants of Tetralogy of Fallot (TOF), the
 CC most common form of complex congenital heart disease.
 CC -!- SIMILARITY: Contains 15 EGF-like domains.
 CC -!- SIMILARITY: Contains 1 DSL domain.
 CC -!- CAUTION: Ref.7 sequence differs from that shown due to a
 CC frameshift in position 1187.
 CC -----
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Query Match 100.0%; Score 1116; DB 1; Length 1218;
 Best Local Similarity 100.0%; Pred. No. 1.7e-96;
 Matches 198; Conservative, 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQGFLEILSMQNYGELQNGCCGARNPGDKTRDECDTYFKVCLKEYQSRVTAGGP 60
 Db 32 SQGFLEILSMQNYGELQNGCCGARNPGDKTRDECDTYFKVCLKEYQSRVTAGGP 91

QY 61 CSFGSGSTPVIGGNTFNKASGRNDRNIVLPFSFAMPRSYTLTLLVEAWDSSNDTVQPDSSI 120
 Db 92 CSFGSGSTPVIGGNTFNKASGRNDRNIVLPFSFAMPRSYTLTLLVEAWDSSNDTVQPDSSI 151

QY 121 IEKASHSGMINPSQWOTLKONTGVAHFEYQIRVTCDDYYGFCNKFRCRDRDDFFGHYA 180
 Db 152 IEKASHSGMINPSQWOTLKONTGVAHFEYQIRVTCDDYYGFCNKFRCRDRDDFFGHYA 211

QY 181 CDQNGNKTCEGWMGPEC 198
 Db 212 CDQNGNKTCEGWMGPEC 229

RESULT 2
 JAGL_RAT STANDARD; PRT; 1219 AA.

AC Q63722; P70640;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Jagged 1 precursor (Jaggedl).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID-10116;
 RN [1]

SEQUENCE FROM N.A.
 RC TISSUE-Sciatic nerve;
 RX MEDLINE=95211842; PubMed=7697721;
 RA Lindell C.E., Shawber C.J., Boulter J., Weinmaster G.;
 RT "Jagged: a mammalian ligand that activates Notchl.,";
 RL Cell 80:909-917(1995).

CC -!- FUNCTION: Ligand for multiple Notch receptors and involved in the
 CC mediation of Notch signaling. May be involved in cell-fate
 CC decisions during hematopoiesis. Enhances fibroblast growth
 CC factor-induced angiogenesis (in vitro). Seems to be involved in
 CC early and late stages of mammalian cardiovascular development.
 CC Inhibits myoblast differentiation. May regulate fibroblast
 CC growth factor-induced angiogenesis.
 CC -!- SUBUNIT: Interacts with NOTCH1, NOTCH2 AND NOTCH3 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Widely expressed in a variety of tissues.
 CC -!- DEVELOPMENTAL STAGE: Expression is seen in E11.5-E14.5 embryos in
 CC four distinct regions of the ventricular zone in the developing
 CC spinal cord.
 CC -!- SIMILARITY: Contains 15 EGF-like domains.
 CC -!- SIMILARITY: Contains 1 DSL domain.

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DR EMBL; L38483; AAB06509.1; -;
 DR HSSP; P00740; 1EDM.
 DR GO; GO:0005576; C:extracellular; ISS.
 DR GO; GO:0005887; C:integral to plasma membrane; ISS.
 DR GO; GO:0008083; F:growth factor activity; ISS.
 DR GO; GO:0005112; F:Notch binding activity; ISS.
 DR GO; GO:0005198; F:structural molecule activity; ISS.
 DR GO; GO:0001525; P:angiogenesis; ISS.

DR GO; GO:0001709; P:cell fate determination; NAS.
 DR GO; GO:0045446; P:endothelial cell differentiation; ISS.
 DR GO; GO:0030097; P:hemoopoiesis; ISS.
 DR GO; GO:0030216; P:keratinocyte differentiation; ISS.
 DR GO; GO:0045445; P:myoblast differentiation; ISS.
 DR GO; GO:0007219; P:N receptor signaling pathway; ISS.
 DR GO; GO:0007399; P:neurogenesis; ISS.
 DR GO; GO:0042127; P:regulation of cell proliferation; ISS.
 DR InterPro; IPR000152; ASx_hydroxyl.
 DR InterPro; IPR001774; DSL.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF01414; DSL; 1.
 DR Pfam; PF00008; EGF; 14.
 DR PRINTS; PR00010; EGFBL00D.
 DR SMART; SM00051; DSL; 1.
 DR SMART; SM00179; EGF_CA; 10.
 DR SMART; SM00214; VWC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 10.
 DR PROSITE; PS00022; EGF_1; 16.
 DR PROSITE; PS01186; EGF_2; 12.
 DR PROSITE; PS01187; EGF_CA; 8.
 DR Calcium-binding; EGF-like domain; Glycoprotein; Developmental protein;
 KW Repeat; Transmembrane; Signal.
 FT SIGNAL; 1 33 POTENTIAL.
 FT CHAIN; 34 1219 JAGGED 1.
 FT DOMAIN; 34 1067 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM; 1068 1093 POTENTIAL.
 FT DOMAIN; 1094 1219 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN; 167 229 DSL.
 FT DOMAIN; 230 266 EGF-LIKE 1 (ATYPICAL).
 FT DOMAIN; 296 334 EGF-LIKE 2.
 FT DOMAIN; 336 372 EGF-LIKE 3.
 FT DOMAIN; 374 410 EGF-LIKE 4.
 FT DOMAIN; 412 448 EGF-LIKE 5.
 FT DOMAIN; 450 485 EGF-LIKE 6.
 FT DOMAIN; 487 523 EGF-LIKE 7.
 FT DOMAIN; 525 561 EGF-LIKE 8.
 FT DOMAIN; 574 627 EGF-LIKE 9.
 FT DOMAIN; 629 665 EGF-LIKE 10.
 FT DOMAIN; 667 703 EGF-LIKE 11.
 FT DOMAIN; 705 741 EGF-LIKE 12.
 FT DOMAIN; 744 780 EGF-LIKE 13.
 FT DOMAIN; 820 856 EGF-LIKE 14.
 FT DOMAIN; 858 896 EGF-LIKE 15.
 FT DISULFID; 300 312 BY SIMILARITY.
 FT DISULFID; 306 322 BY SIMILARITY.
 FT DISULFID; 324 333 BY SIMILARITY.
 FT DISULFID; 340 351 BY SIMILARITY.
 FT DISULFID; 345 360 BY SIMILARITY.
 FT DISULFID; 362 371 BY SIMILARITY.
 FT DISULFID; 378 389 BY SIMILARITY.
 FT DISULFID; 383 398 BY SIMILARITY.
 FT DISULFID; 400 409 BY SIMILARITY.
 FT DISULFID; 416 427 BY SIMILARITY.
 FT DISULFID; 421 436 BY SIMILARITY.
 FT DISULFID; 438 447 BY SIMILARITY.
 FT DISULFID; 454 464 BY SIMILARITY.
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 FT DISULFID; 491 502 BY SIMILARITY.
 FT DISULFID; 496 511 BY SIMILARITY.
 FT DISULFID; 513 522 BY SIMILARITY.
 FT DISULFID; 529 540 BY SIMILARITY.
 FT DISULFID; 534 549 BY SIMILARITY.
 FT DISULFID; 551 560 BY SIMILARITY.
 FT DISULFID; 578 605 BY SIMILARITY.
 FT DISULFID; 599 615 BY SIMILARITY.
 FT DISULFID; 617 626 BY SIMILARITY.
 FT DISULFID; 633 644 BY SIMILARITY.

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FT DISULFID 638 653 BY SIMILARITY.
FT DISULFID 655 664 BY SIMILARITY.
FT DISULFID 671 682 BY SIMILARITY.
FT DISULFID 676 691 BY SIMILARITY.
FT DISULFID 693 702 BY SIMILARITY.
FT DISULFID 709 720 BY SIMILARITY.
FT DISULFID 714 729 BY SIMILARITY.
FT DISULFID 731 740 BY SIMILARITY.
FT DISULFID 748 759 BY SIMILARITY.
FT DISULFID 753 768 BY SIMILARITY.
FT DISULFID 770 779 BY SIMILARITY.
FT DISULFID 786 797 BY SIMILARITY.
FT DISULFID 791 806 BY SIMILARITY.
FT DISULFID 808 817 BY SIMILARITY.
FT DISULFID 824 835 BY SIMILARITY.
FT DISULFID 829 844 BY SIMILARITY.
FT DISULFID 846 855 BY SIMILARITY.
FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 217 217 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 559 559 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 745 745 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 960 960 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 991 991 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1045 1045 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1064 1064 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1219 AA; 134325 MW; 65D4CFC38A0E204 CRC64;

Query Match 99.4%; Score 1109; DB 1; Length 1219;
Best Local Similarity 98.5%; Pred. No. 7.8e-96;
Matches 195; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGQFEILLSMQNVGELONGCCGARNPGDRKCTRDCEDTYFKVCLKEYOSRVTAGGP 60
DB 32 SQQFEILLSMQNVGELONGCCGARNPGDRKCTRDCEDTYFKVCLKEYOSRVTAGGP 91

QY 61 CSFGSGSTPVIGGNTFNLSKASGRNDRNRLVLPFSFAWPRSYYTLLEAWDSSNDTVQPSI 120
DB 92 CSFGSGSTPVIGGNTFNLSKASGRNDRNRLVLPFSFAWPRSYYTLLEAWDSSNDTVQPSI 151

QY 121 IEKASHGMINPSROWTILKQNTGVAFHYQIRVTCDDYYHYGCGNKFRCRDRDDFGHYA 180
DB 152 IEKASHGMINPSROWTILKQNTGVAFHYQIRVTCDDYYHYGCGNKFRCRDRDDFGHYA 211

QY 181 CDQNGNKTCEMGWGPEC 198
DB 212 CDQNGNKTCEMGWGPEC 229

RESULT 3
JAGL_MOUSE STANDARD; PRT; 1218 AA.
AC Q90XX0:
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Jagged 1 precursor (Jagged1).
GN JAG1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A., AND RECEPTOR INTERACTION.
RC STRAIN=Swiss Webster / NIH;
RX MEDLINE=20020271; PubMed=10551863;
RA Shimizu K., Chiba S., Kumano K., Hosoya N., Takahashi T., Kanda Y.,
RA Hamada Y., Yazaki Y., Hirai H.;
RT "Mouse Jagged1 physically interacts with Notch2 and other Notch
RT receptors: assessment by quantitative methods.";
RL J. Biol. Chem. 274:32961-32969(1999).
RN [2]
RP TISSUE SPECIFICITY.
```

```
RX MEDLINE=20025753; PubMed=10556292;
RA Loomes K.M., Underkoffler L.A., Morabito J., Gottlieb S.,
RA Piccoli D.A., Spinner N.B., Baldwin H.S., Oakey R.J.;
RT "The expression of Jagged1 in the developing mammalian heart
RT correlates with cardiovascular disease in Alagille syndrome.";
RL Hum. Mol. Genet. 8:2443-2449(1999).
CC -!- FUNCTION: Ligand for multiple Notch receptors and involved in the
CC mediation of Notch signaling. May be involved in cell-fate
CC decisions during hematopoiesis. Seems to be involved in early
CC and late stages of mammalian cardiovascular development. Inhibits
CC myoblast differentiation (By similarity). May regulate fibroblast
CC growth factor-induced angiogenesis.
CC -!- SUBUNIT: Interacts with NOTCH1, NOTCH2 AND NOTCH3.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Widely expressed in many tissues, with highest
CC expression in brain, heart, muscle and thymus.
CC -!- DEVELOPMENTAL STAGE: At 8.75-9.75 dpc expression was detected
CC in structures that include those destined to contribute to the
CC cardiovascular system of the adult heart. Expression was also
CC detected in the mesencephalon and rhombencephalon.
CC -!- DOMAIN: The DSL domain is indispensable and sufficient for binding
CC to NOTCH2.
CC -!- SIMILARITY: Contains 15 EGF-like domains.
CC -!- SIMILARITY: Contains 1 DSL domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF171092; AAF15505.1; -
CC HSSP: P00740; IEDM.
CC MGD: MGI:1095416; Jag1.
CC GO: GO:0005576; C:extracellular; ISS.
CC GO: GO:0005509; F:calcium ion binding activity; NAS.
CC GO: GO:0008083; F:growth factor activity; ISS.
CC GO: GO:0005112; F:Notch binding activity; IPI.
CC GO: GO:0005198; F:structural molecule activity; ISS.
CC GO: GO:0001525; P:angiogenesis; ISS.
CC GO: GO:0001709; P:cell fate determination; ISS.
CC GO: GO:0045446; P:endothelial cell differentiation; ISS.
CC GO: GO:0030097; P:hemopoiesis; ISS.
CC GO: GO:0002011; P:keratinocyte differentiation; ISS
CC GO: GO:0002016; P:morphogenesis of an epithelial sheet; IMP.
CC GO: GO:0043445; P:myoblast differentiation; ISS.
CC GO: GO:0007219; P:N receptor signaling pathway; ISS.
CC GO: GO:0007399; P:neurogenesis; ISS.
CC GO: GO:0042127; P:regulation of cell proliferation; ISS.
CC InterPro: IPR000152; Asx_hydroxyl.
CC InterPro: IPR001774; DSL.
CC InterPro: IPR000742; EGF_2.
CC InterPro: IPR001881; EGF_CA.
CC InterPro: IPR001438; EGF_II.
CC InterPro: IPR006209; EGF_like.
CC InterPro: IPR001007; VWF_C.
CC Pfam: PF01414; DSL; 1.
CC Pfam: PF00008; EGF; 14.
CC PRINTS: PR00010; EGFBL00D.
CC SMART: SM00051; DSL; 1.
CC SMART: SM00179; EGF_CA; 10.
CC SMART: SM00214; VWC; 1.
CC PROSITE: PS00010; ASX_HYDROXYL; 10.
CC PROSITE: PS00022; EGF_1; 16.
CC PROSITE: PS01186; EGF_2; 12.
CC PROSITE: PS01187; EGF_CA; 8.
CC Repeat; Transmembrane; Signal.
KW Calcium-binding; EGF-like domain; Glycoprotein; Developmental protein;
KW Repeat; Transmembrane; Signal.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 1218 JAGGED 1.
FT DOMAIN 34 1067 EXTRACELLULAR (POTENTIAL).
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FT	TRANSMEM	1068	1093	POTENTIAL.		Matches	193;	Conservative	4;	Mismatches	1;	Indels	0;	Gaps	0;
FT	DOMAIN	1094	1218	CYTOPLASMIC (POTENTIAL).		QY	1	SGQFEILSLMQNVNCGELONGCCGGARNPGRKCTDECDTYFKVCLKEVQSVRTAGGP	60						
FT	DOMAIN	167	229	DSL.		Db	32	SGQFEILSLMQNVNCGELONGCCGGVRNPGDRKCTDECDTYFKVCLKEVQSVRTAGGP	91						
FT	DOMAIN	230	266	EGF-LIKE 1 (ATYPICAL).											
FT	DOMAIN	296	334	EGF-LIKE 2.											
FT	DOMAIN	336	372	EGF-LIKE 3.											
FT	DOMAIN	374	410	EGF-LIKE 4.	CALCIUM-BINDING (POTENTIAL).	QY	61	CSFGSGSTPVIGGNTFNKASRGNDNRNRIVLPSFAWPRSYTLLEAVEWSSNDTVQPDSSI	120						
FT	DOMAIN	412	448	EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).		Db	92	CSFGSGSTPVIGGNTFNKASRGNDNRNRIVLPSFAWPRSYTLLEAVEWSSNDTVQPDSSI	151						
FT	DOMAIN	450	485	EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).											
FT	DOMAIN	487	523	EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).		QY	121	IERASHSGMNPQRQWOTLKQNTGVAHFYQIRVTCDDYYGFGCNKFCPRDDFFGHYA	180						
FT	DOMAIN	525	561	EGF-LIKE 8.		Db	152	IERASHSGMNPQRQWOTLKQNTGVAHFYQIRVTCDDYYGFGCNKFCPRDDFFGHYA	211						
FT	DOMAIN	574	627	EGF-LIKE 9.		QY	181	CDQNGNKTCEGWMGPEC	198						
FT	DOMAIN	629	665	EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).		Db	212	CDQNGNKTCEGWMGPDC	229						
FT	DOMAIN	667	703	EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).											
FT	DOMAIN	705	741	EGF-LIKE 12.											
FT	DOMAIN	744	780	EGF-LIKE 13.											
FT	DOMAIN	782	818	EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).											
FT	DOMAIN	820	856	EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).											
FT	DISULFID	300	312	BY SIMILARITY.											
FT	DISULFID	306	322	BY SIMILARITY.											
FT	DISULFID	324	333	BY SIMILARITY.											
FT	DISULFID	340	351	BY SIMILARITY.											
FT	DISULFID	345	360	BY SIMILARITY.											
FT	DISULFID	362	371	BY SIMILARITY.											
FT	DISULFID	378	389	BY SIMILARITY.											
FT	DISULFID	383	398	BY SIMILARITY.											
FT	DISULFID	400	409	BY SIMILARITY.											
FT	DISULFID	416	427	BY SIMILARITY.											
FT	DISULFID	421	436	BY SIMILARITY.											
FT	DISULFID	438	447	BY SIMILARITY.											
FT	DISULFID	454	464	BY SIMILARITY.											
FT	DISULFID	458	473	BY SIMILARITY.											
FT	DISULFID	475	484	BY SIMILARITY.											
FT	DISULFID	491	502	BY SIMILARITY.											
FT	DISULFID	496	511	BY SIMILARITY.											
FT	DISULFID	513	522	BY SIMILARITY.											
FT	DISULFID	529	540	BY SIMILARITY.											
FT	DISULFID	534	549	BY SIMILARITY.											
FT	DISULFID	551	560	BY SIMILARITY.											
FT	DISULFID	578	605	BY SIMILARITY.											
FT	DISULFID	599	615	BY SIMILARITY.											
FT	DISULFID	617	626	BY SIMILARITY.											
FT	DISULFID	633	644	BY SIMILARITY.											
FT	DISULFID	638	653	BY SIMILARITY.											
FT	DISULFID	655	664	BY SIMILARITY.											
FT	DISULFID	671	682	BY SIMILARITY.											
FT	DISULFID	676	691	BY SIMILARITY.											
FT	DISULFID	693	702	BY SIMILARITY.											
FT	DISULFID	709	720	BY SIMILARITY.											
FT	DISULFID	714	729	BY SIMILARITY.											
FT	DISULFID	731	740	BY SIMILARITY.											
FT	DISULFID	748	759	BY SIMILARITY.											
FT	DISULFID	753	768	BY SIMILARITY.											
FT	DISULFID	770	779	BY SIMILARITY.											
FT	DISULFID	786	797	BY SIMILARITY.											
FT	DISULFID	791	806	BY SIMILARITY.											
FT	DISULFID	808	817	BY SIMILARITY.											
FT	DISULFID	824	835	BY SIMILARITY.											
FT	DISULFID	829	844	BY SIMILARITY.											
FT	DISULFID	846	855	BY SIMILARITY.											
FT	CARBOHYD	143	143	N-LINKED (GLCNAC. . .) (POTENTIAL).											
FT	CARBOHYD	217	217	N-LINKED (GLCNAC. . .) (POTENTIAL).											
FT	CARBOHYD	382	382	N-LINKED (GLCNAC. . .) (POTENTIAL).											
FT	CARBOHYD	559	559	N-LINKED (GLCNAC. . .) (POTENTIAL).											
FT	CARBOHYD	745	745	N-LINKED (GLCNAC. . .) (POTENTIAL).											
FT	CARBOHYD	960	960	N-LINKED (GLCNAC. . .) (POTENTIAL).											
FT	CARBOHYD	991	991	N-LINKED (GLCNAC. . .) (POTENTIAL).											
FT	CARBOHYD	1045	1045	N-LINKED (GLCNAC. . .) (POTENTIAL).											
FT	CARBOHYD	1064	1064	N-LINKED (GLCNAC. . .) (POTENTIAL).											
SQ	SEQUENCE	1218 AA;	134163 MW;	77739F8928B793C CRC64;											

Query Match 98.7%; Score 1102; DB 1; Length 1218;
Best Local Similarity 97.5%; Pred. No. 3.5e-95;

RESULT 4

JAG3_BRARE	STANDARD;	PRT;	1213 AA.
ID	JAG3_BRARE		
AC	Q90Y54;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Jagged 3 precursor (Jagged3).		
GN	JAG3.		
OS	Brachydanio rerio (zebrafish) (Danio rerio).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;		
OC	Cyprinidae; Danio.		
OX	NCBI_TaxID=7955;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RA	Oda T., Chandrasekharappa S.C.;		
RT	"Isolation, characterization and expression analysis of zebrafish		
RT	Jagged genes."		
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.		
CC	-!- FUNCTION: Ligand for Notch receptors and involved in the mediation		
CC	of Notch signaling (By similarity). Seems to be involved in cell-		
CC	fate decisions.		
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).		
CC	-!- SIMILARITY: Contains 17 EGF-like domains.		
CC	-!- SIMILARITY: Contains 1 DSL domain.		
CC	-!- SIMILARITY: Contains 1 WFC domain.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; AF229451; AAL08216.1; .		
DR	ZFIN; ZDB-GENE-011128-4; jag3.		
DR	InterPro; IPR000152; Asx_hydroxyl.		
DR	InterPro; IPR001774; DSL.		
DR	InterPro; IPR000742; EGF-2.		
DR	InterPro; IPR001881; EGF-Ca.		
DR	InterPro; IPR001438; EGF-II.		
DR	InterPro; IPR006209; EGF-like.		
DR	InterPro; IPR002049; Laminin_EGF.		
DR	Pfam; PF01414; DSL; 1.		
DR	Pfam; PF00008; EGF; 14.		
DR	PRINTS; PR00010; EGFBL00D.		
DR	PRINTS; PR00011; EGFAMININ.		
DR	SMART; SM00051; DSL; 1.		
DR	SMART; SM00179; EGF_CA; 10.		
DR	SMART; SM00214; WVC; 1.		
DR	PROSITE; PS00010; ASX_HYDROXYL; 10.		

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DR PROSITE; PS00022; EGF_1; 16.
DR PROSITE; PS01186; EGF_2; 12.
DR PROSITE; PS01187; EGF_CA; 8.
DR PROSITE; PS01208; WFC_1; FALSE_NEG.
KW Calcium-binding; EGF-like domain; Glycoprotein; Developmental protein;
KW Repeat; Transmembrane; Signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 1213 JAGGED 3.
FT DOMAIN 27 1064 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1065 1087 POTENTIAL.
FT DOMAIN 1088 1213 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 164 226 DSL.
FT DOMAIN 227 260 EGF-LIKE 1.
FT DOMAIN 258 291 EGF-LIKE 2.
FT DOMAIN 293 331 EGF-LIKE 3.
FT DOMAIN 333 369 EGF-LIKE 4.
FT DOMAIN 371 407 EGF-LIKE 5.
FT DOMAIN 409 445 EGF-LIKE 6.
FT DOMAIN 447 482 EGF-LIKE 7.
FT DOMAIN 484 520 EGF-LIKE 8.
FT DOMAIN 522 558 EGF-LIKE 9.
FT DOMAIN 592 624 EGF-LIKE 10.
FT DOMAIN 626 662 EGF-LIKE 11.
FT DOMAIN 664 700 EGF-LIKE 12.
FT DOMAIN 702 738 EGF-LIKE 13.
FT DOMAIN 746 777 EGF-LIKE 14.
FT DOMAIN 779 815 EGF-LIKE 15.
FT DOMAIN 817 853 EGF-LIKE 16.
FT DOMAIN 860 914 VMC.
FT DOMAIN 918 956 EGF-LIKE 17.
FT DISULFID 231 242 BY SIMILARITY.
FT DISULFID 235 248 BY SIMILARITY.
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FT DISULFID 262 273 BY SIMILARITY.
FT DISULFID 268 279 BY SIMILARITY.
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FT DISULFID 337 348 BY SIMILARITY.
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FT DISULFID 493 508 BY SIMILARITY.
FT DISULFID 510 519 BY SIMILARITY.
FT DISULFID 526 537 BY SIMILARITY.
FT DISULFID 531 546 BY SIMILARITY.
FT DISULFID 548 557 BY SIMILARITY.
FT DISULFID 530 641 BY SIMILARITY.
FT DISULFID 635 650 BY SIMILARITY.
FT DISULFID 652 661 BY SIMILARITY.
FT DISULFID 668 679 BY SIMILARITY.
FT DISULFID 673 688 BY SIMILARITY.
FT DISULFID 690 699 BY SIMILARITY.
FT DISULFID 706 717 BY SIMILARITY.
FT DISULFID 711 726 BY SIMILARITY.
FT DISULFID 728 737 BY SIMILARITY.
FT DISULFID 783 794 BY SIMILARITY.
FT DISULFID 788 803 BY SIMILARITY.
FT DISULFID 805 814 BY SIMILARITY.
FT DISULFID 821 832 BY SIMILARITY.
FT DISULFID 826 841 BY SIMILARITY.
FT DISULFID 843 852 BY SIMILARITY.
FT DOMAIN 938 941 POLY-PRO.

FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 214 214 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 556 556 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 742 742 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 957 957 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 988 988 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1042 1042 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 1213 AA; 133365 MW; 5C5F16A7E20D9534 CRC64;

Query Match 76.1%; Score 849; DB 1; Length 1213;
Best Local Similarity 75.4%; Pred. No. 1.6e-71;
Matches 150; Conservative 21; Mismatches 26; Indels 2; Gaps 2;

QY 1 SGQFEILLSMONVANGELONGNCCGARNPDRKCTDECDYFKVCLKEYQSRVTAGP 60
DB 29 SGHFEILLSMONANGELONGACCDGARNPARDKCTDECDYFKVCLKEYQSRVSAGA 88
QY 61 CSFGSGSTPVIGGNTFNFKASGRNDRNRLVLPFSFAMPRSYTLVLEAWDSSNDTV-OPDS 119
DB 89 CSFGTGSTPVLGNKFSTKGR-SEKSRVLVLPFSFAMPRSYTLVLEALDFNNETASESG 147
QY 120 IIEKASHSGMINPSRQWQTLKONTGVAHEFYQIRVTCDDYVYGFSGCNKFCRPRDFFGHY 179
DB 148 LIEKAYHSGMINPNRQWQLTHNGPVAQFEYQIRVTCLEHYVYGFSGCNKFCRPRDFFGHY 207
QY 180 ACDQNGKTKCMGWMGPEC 198
DB 208 TCDQNGKTKLEGWTGPDC 226

RESULT 5
JAG1_BRARE
ID JAG1_BRARE STANDARD; PRT; 1242 AA.
AC Q90Y57;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Jagged 1 precursor (Jagged1).
GN JAG1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Oda T., Chandrasekharappa S.C.;
RT "Isolation, characterization and expression analysis of Zebrafish
  Jagged genes.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ligand for multiple Notch receptors and involved in the
  mediation of Notch signaling (by similarity). Seems to be involved
  in cell-fate decisions.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Contains 17 EGF-like domains.
CC -!- SIMILARITY: Contains 1 DSL domain.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF229448; AAL08213.1; -.
DR ZFIN; ZDB-GENE-011128-2; Jag1.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002049; Laminin_EGF.
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DR InterPro: IPR001007; VWF_C.
DR Pfam: PF01414; DSL; 1.
DR Pfam: PF00008; EGF; 14.
DR PRINTS: PR00011; EGFAMININ.
DR SMART: SM00051; DSL; 1.
DR SMART: SM00179; EGF_CA; 9.
DR SMART: SM00214; VWC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 9.
DR PROSITE: PS00022; EGF_1; 16.
DR PROSITE: PS01186; EGF_2; 12.
DR PROSITE: PS01187; EGF_CA; 8.
KW Calcium-binding; EGF-like domain; Glycoprotein; Developmental protein;
KW Repeat; Transmembrane; Signal.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 1242 JAGGED 1.
FT DOMAIN 29 1070 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1071 1095 POTENTIAL.
FT DOMAIN 1096 1242 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 168 230 DSL.
FT DOMAIN 231 264 EGF-LIKE 1.
FT DOMAIN 262 295 EGF-LIKE 2.
FT DOMAIN 297 335 EGF-LIKE 3.
FT DOMAIN 337 373 EGF-LIKE 4.
FT DOMAIN 375 411 EGF-LIKE 5.
FT DOMAIN 413 449 EGF-LIKE 6.
FT DOMAIN 451 486 EGF-LIKE 7.
FT DOMAIN 488 524 EGF-LIKE 8.
FT DOMAIN 526 562 EGF-LIKE 9.
FT DOMAIN 575 630 EGF-LIKE 10.
FT DOMAIN 632 668 EGF-LIKE 11.
FT DOMAIN 670 706 EGF-LIKE 12.
FT DOMAIN 708 744 EGF-LIKE 13.
FT DOMAIN 747 783 EGF-LIKE 14.
FT DOMAIN 785 821 EGF-LIKE 15.
FT DOMAIN 823 859 EGF-LIKE 16.
FT DOMAIN 859 917 EGF-LIKE 17.
FT DISULFID 235 246 BY SIMILARITY.
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FT DISULFID 459 474 BY SIMILARITY.
FT DISULFID 476 485 BY SIMILARITY.
FT DISULFID 492 503 BY SIMILARITY.
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FT DISULFID 530 541 BY SIMILARITY.
FT DISULFID 535 550 BY SIMILARITY.
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FT DISULFID 636 647 BY SIMILARITY.
FT DISULFID 641 656 BY SIMILARITY.
FT DISULFID 658 667 BY SIMILARITY.
FT DISULFID 674 685 BY SIMILARITY.
FT DISULFID 679 694 BY SIMILARITY.
FT DISULFID 696 705 BY SIMILARITY.
FT DISULFID 712 723 BY SIMILARITY.
FT DISULFID 717 732 BY SIMILARITY.
FT DISULFID 734 743 BY SIMILARITY.
FT DISULFID 751 762 BY SIMILARITY.

FT DISULFID 756 771 BY SIMILARITY.
FT DISULFID 773 782 BY SIMILARITY.
FT DISULFID 789 800 BY SIMILARITY.
FT DISULFID 794 809 BY SIMILARITY.
FT DISULFID 811 820 BY SIMILARITY.
FT DISULFID 827 838 BY SIMILARITY.
FT DISULFID 832 847 BY SIMILARITY.
FT DISULFID 849 858 BY SIMILARITY.
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 218 218 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 560 560 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 960 960 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 991 991 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1046 1046 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1242 AA; 135343 MW; 59557A4B7F052860 CRC64;

Query Match 74.4%; Score 830; DB 1; Length 1242;
Best Local Similarity 71.3%; Pred. No. 9.8e-70;
Matches 144; Conservative 26; Mismatches 28; Indels 4; Gaps 2;

QY 1 SGOFELILSMQNVGELQNGCCGARNPGRKTRDECDYFKVCLKEYQSRVATGGP 60
Db 29 SGHFENQVLSMQNVGELQSGACCDGARDPAERSCAADQCDTFRVCLEKEYQSRVSSGGP 88
QY 61 CSFGSGSTPVIGGNTFNLK-ASRGNDNRNRLVLPFSFAWPRSYTLVLEAWDSSNDTVQPD- 118
Db 89 CSYGSGSTPVIGGNTFVSVKPLDQTNKTRIVLPFSFAWPRSYTLVLEALDFNDSSTGSI 148
QY 119 --SIIEKASHSGMINPSROWQTLKONTGVAHFYQIRVTCDDYVYFGCNKFCRPRDDFF 176
Db 149 NGQVIEKAVQSGMINPNRQWVLKNGPVAQFQYQIRVTCDEHYFGCNKFCRPRDDFF 208
QY 177 GHYACDQNGKTCMEGWMGPEC 198
Db 209 GHYTCDHNGNKTCLEGWAGPEC 230

RESULT 6
JAG2_MOUSE STANDARD; PRT; 1247 AA.
AC O9QVE5; O55139; 070219;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Jagged 2 precursor (Jagged2).
GN JAG2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster / NIH;
RA Tsai S.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 302-819 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98051918; PubMed=93411252;
RA Lan Y., Jiang R., Shawber C., Weinmaster G., Gridley T.;
RT "The Jagged2 gene maps to chromosome 12 and is a candidate for the lgl
RT and sm mutations.";
RL Mamm. Genome 8:875-876(1997).
RN [3]
RP SEQUENCE OF 325-759 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98145947; PubMed=9486542;
RA Valsecchi C., Ghezzi C., Ballabio A., Rugarli E.I.;
RT "JAGGED2: a putative Notch ligand expressed in the apical ectodermal
RT ridge and in sites of epithelial-mesenchymal interactions.";
RL Mech. Dev. 69:203-207(1997).
```


FT CARBOHYD 1060 1060 N-LINKED (GLNAC...) (POTENTIAL).
FT CONFLICT 302 302 L -> M (IN REF. 2).
FT CONFLICT 461 461 N -> T (IN REF. 2).
FT CONFLICT 469 478 CQHGCTCKDL -> VSAWGHQGP (IN REF. 2).
FT CONFLICT 492 492 G -> V (IN REF. 2).
FT CONFLICT 546 546 L -> F (IN REF. 2).
FT CONFLICT 549 549 A -> V (IN REF. 2).
FT CONFLICT 735 738 RCAC -> PAR (IN REF. 3).
FT CONFLICT 809 809 N -> H (IN REF. 2).
FT CONFLICT 812 812 R -> A (IN REF. 2).
SQ SEQUENCE 1247 AA; 134726 MW; 1D80C8626FAAEEC CRC64;

Query Match
Best Local Similarity 59.1%; Score 659; DB 1; Length 1247;
Matches 122; Conservative 27; Mismatches 47; Indels 18; Gaps 5;

QY 2 GQFELELLSMQVNGELQNGCC-GGARNPGDKRTRDECDTFKVLCKEYQSRVTAGGP 60
Dy 28 GFYELQLSALRNVNGELLSGCCDGGRTTRAGCGRDECDTVYRVCLKEYQAKVTPTGP 87
QY 61 CSFGSGSTPVIGGNTFL-KASRGNDNR-----IVLPFSFAWPRSYTLLE 106
Dy 88 CSYGYGATPVLGNSFVLPAGAGDRARSRRTGGHDPGLVVPFQFAWPRSYTLLE 147

QY 107 AWDSNDTVPQDS--IIKASHSGMINPSQWTLKONTGVAHFYQIRVTCDDYYXGFG 164
Dy 148 AWDNDDTT-PDELLIYRVSHAGMINPDRWKSLSHFSGHVAHLEQLIRVRCDENYYSAT 206

QY 165 CNKFCRPRDDFFGHYACDQNGKTCMEGWMGPEC 198
Dy 207 CNKFCRPRDDFFGHYTCQYGNKACMDGWMGKEC 240

RESULT 7
JAG2_HUMAN
ID JAG2_HUMAN STANDARD; PRT; 1238 AA.
AC Q9Y219; Q9UE17; Q9UE99; Q9UNK8; Q9Y6P9; Q9Y6Q0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Jagged 2 precursor (Jagged2) (HJ2).
GN JAG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RX MEDLINE=97459705; PubMed=9315665;
RA Luo B., Aster J.C., Hasserjian R.P., Kuo F., Sklar J.;
RT "Isolation and functional analysis of a cDNA for human Jagged2, a gene
RL encoding a ligand for the Notch1 receptor.";
RL Mol. Cell. Biol. 17:6057-6067(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RX TISSUE=Fetal brain;
RC TISSUE=Fetal brain;
RX MEDLINE=99180765; PubMed=10079256;
RA Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
RT "Human ligands of the Notch receptor.";
RL Am. J. Pathol. 154:785-794(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC TISSUE=Bone marrow;
RX MEDLINE=20130121; PubMed=10662552;
RA Deng Y., Madan A., Banta A.B., Friedman C., Trask B.J., Hood L.,
RA Li L.;
RT "Characterization, chromosomal localization, and the complete 30-kb
RL DNA sequence of the human Jagged2 (JAG2) gene.";
RN Genomics 63:133-138(2000).
RP [4]
RC SEQUENCE OF 17-1238 FROM N.A. (ISOFORM LONG).
RC TISSUE=Heart;

RX MEDLINE=98145947; PubMed=9486542;
RA Valsecchi C., Ghezzi C., Ballabio A., Rugarli E.I.;
RT "JAGGED2: a putative Notch ligand expressed in the apical ectodermal
RL ridge and in sites of epithelial-mesenchymal interactions.";
RL Mech. Dev. 69:203-207(1997).
CC -1- FUNCTION: PUTATIVE NOTCH LIGAND INVOLVED IN THE MEDIATION OF NOTCH
CC SIGNALING. INVOLVED IN LIMB DEVELOPMENT (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q9Y219-1; Sequence=Displayed;
CC Name=Short; Synonyms=HJAG2.del-B6;
CC IsoId=Q9Y219-2; Sequence=VSP_001395;
CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, PLACENTA AND SKELETAL
CC MUSCLE AND TO A LESSER EXTENT IN PANCREAS. VERY LOW EXPRESSION IN
CC BRAIN, LUNG, LIVER AND KIDNEY.
CC -1- DISEASE: MAY BE ASSOCIATED TO USHER SYNDROME TYPE IA (USH1A)
CC WHICH DESCRIBES A CONGENITAL SENSORY DEAFNESS ASSOCIATED WITH
CC RETINITIS PIGMENTOSA AND FEEBLE-MINDEDNESS.
CC -1- SIMILARITY: Contains 16 EGF-like domains.
CC -1- SIMILARITY: Contains 1 DSL domain.
CC -1- SIMILARITY: Contains 1 VWC domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF020201; AAB71189.1; -;
DR EMBL; AF003521; AAB61285.1; -;
DR EMBL; AF029778; AAB84215.1; -;
DR EMBL; AF029779; AAB84216.1; -;
DR EMBL; AF111170; AAD1562.1; -;
DR EMBL; Y14330; CAA74706.1; -;
DR HSSP; P00743; ICCF.
DR Genew; HGNC:6189; JAG2.
DR MIM; 602370; -;
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0008083; F:growth factor activity; IDA.
DR GO; GO:0005112; F:Notch binding activity; IPI.
DR GO; GO:0007049; P:cell cycle; NAS.
DR GO; GO:0030154; P:cell differentiation; IDA.
DR GO; GO:0001709; P:cell fate determination; NAS.
DR GO; GO:0007267; P:cell-cell signaling; ISS.
DR GO; GO:0009912; P:hair cell fate commitment; ISS.
DR GO; GO:0007605; P:hearing; ISS.
DR GO; GO:0030326; P:limb morphogenesis; ISS.
DR GO; GO:0007219; P:N receptor signaling pathway; NAS.
DR GO; GO:0042127; P:regulation of cell migration; NAS.
DR GO; GO:0007283; P:spermatogenesis; IEP.
DR GO; GO:0030217; P:T-cell differentiation; IDA.
DR GO; GO:0045061; P:thymic T-cell selection; IDA.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF-II.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 14.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 9.
DR SMART; SM00214; VWC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 10.
DR PROSITE; PS00022; EGF_1; 16.
DR PROSITE; PS01186; EGF_2; 12.

DR PROSITE; PS01187; EGF_CA; 7.
DR PROSITE; PS01184; WFC2; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Developmental protein;
Repeat; Signal; Transmembrane; Alternative splicing.
FT CHAIN 1 26 POTENTIAL.
FT CHAIN 27 1238 JAGGED 2.
FT TRANSMEM 1081 1105 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 1106 1238 POTENTIAL.
FT DOMAIN 178 240 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 241 274 DSL.
FT DOMAIN 275 305 EGF-LIKE 1.
FT DOMAIN 307 345 EGF-LIKE 2.
FT DOMAIN 347 383 EGF-LIKE 3.
FT DOMAIN 385 421 EGF-LIKE 4.
FT DOMAIN 423 459 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 461 496 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 498 534 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 536 572 EGF-LIKE 8.
FT DOMAIN 574 634 EGF-LIKE 9.
FT DOMAIN 636 672 EGF-LIKE 10 (ATYPICAL).
FT DOMAIN 674 710 EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 712 748 EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 751 787 EGF-LIKE 13.
FT DOMAIN 789 825 EGF-LIKE 14.
FT DOMAIN 827 863 EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 865 901 EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 903 944 WFC.
FT DISULFID 245 256 BY SIMILARITY.
FT DISULFID 258 262 BY SIMILARITY.
FT DISULFID 264 273 BY SIMILARITY.
FT DISULFID 276 287 BY SIMILARITY.
FT DISULFID 289 293 BY SIMILARITY.
FT DISULFID 295 304 BY SIMILARITY.
FT DISULFID 311 323 BY SIMILARITY.
FT DISULFID 325 333 BY SIMILARITY.
FT DISULFID 335 344 BY SIMILARITY.
FT DISULFID 346 352 BY SIMILARITY.
FT DISULFID 354 362 BY SIMILARITY.
FT DISULFID 364 371 BY SIMILARITY.
FT DISULFID 373 382 BY SIMILARITY.
FT DISULFID 384 400 BY SIMILARITY.
FT DISULFID 394 409 BY SIMILARITY.
FT DISULFID 411 420 BY SIMILARITY.
FT DISULFID 422 438 BY SIMILARITY.
FT DISULFID 440 447 BY SIMILARITY.
FT DISULFID 449 458 BY SIMILARITY.
FT DISULFID 465 475 BY SIMILARITY.
FT DISULFID 469 484 BY SIMILARITY.
FT DISULFID 486 495 BY SIMILARITY.
FT DISULFID 502 513 BY SIMILARITY.
FT DISULFID 507 522 BY SIMILARITY.
FT DISULFID 524 533 BY SIMILARITY.
FT DISULFID 534 551 BY SIMILARITY.
FT DISULFID 545 551 BY SIMILARITY.
FT DISULFID 562 571 BY SIMILARITY.
FT DISULFID 589 612 POTENTIAL.
FT DISULFID 606 622 BY SIMILARITY.
FT DISULFID 624 633 BY SIMILARITY.
FT DISULFID 640 651 BY SIMILARITY.
FT DISULFID 645 660 BY SIMILARITY.
FT DISULFID 662 671 BY SIMILARITY.
FT DISULFID 678 689 BY SIMILARITY.
FT DISULFID 693 698 BY SIMILARITY.
FT DISULFID 700 709 BY SIMILARITY.
FT DISULFID 716 727 BY SIMILARITY.
FT DISULFID 721 736 BY SIMILARITY.
FT DISULFID 738 747 BY SIMILARITY.
FT DISULFID 755 766 BY SIMILARITY.
FT DISULFID 760 775 BY SIMILARITY.
FT DISULFID 777 786 BY SIMILARITY.
FT DISULFID 793 804 BY SIMILARITY.
FT DISULFID 798 813 BY SIMILARITY.
FT DISULFID 824 831 BY SIMILARITY.
FT DISULFID 831 842 BY SIMILARITY.

FT DISULFID 836 851 BY SIMILARITY.
FT DISULFID 853 862 BY SIMILARITY.
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 570 570 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 619 619 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 752 752 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1058 1058 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 424 461 Missing (in isoform Short).
FT CONFLICT 8 12 /FTID-VSP_001395.
FT CONFLICT 119 119 RUPRR -> AFPPA (IN REF. 1).
FT CONFLICT 129 129 A -> P (IN REF. 1).
FT CONFLICT 384 384 L -> F (IN REF. 1).
FT CONFLICT 424 426 L -> SA (IN REF. 4).
FT CONFLICT 501 501 ANE -> VND (IN REF. 1).
FT CONFLICT 501 501 K -> E (IN REF. 3; AAD15562 AND 4).
FT CONFLICT 1235 1235 A -> V (IN REF. 2).

Query Match 58.4%; Score 652; DB 1; Length 1238;
Best Local Similarity 55.4%; Pred. No. 4.4e-53;
Matches 118; Conservative 31; Mismatches 48; Indels 16; Gaps 4;
QY 2 GQFEILSMQNVGELQNGCC-GGARNPGRKCTRDCECDYFKVCLKEYQSRVTAGP 60
DB 28 GYFELQLSALRVNGELLSGACDGDGRTRAGCGHDECDYVVRVCLKEYQAKVTPGP 87
QY 61 CSFGSGSTVIGGTFNL-----KASRGNDNRN--RIVLPFSFAPRSTYLLVE 106
DB 88 CSYGHGATVPLGNSFYLPPAGAADRARARAGDQDPLGVVIFQFAPRSTYLLVE 147
QY 107 AWDSSNDTV-OPDSIIKASHGMINPSQWTLKONTGVAHFEYQIRVTCDDYVYFGC 165
DB 148 AWDNDNDTTPNEELLIERVSHAGMINPEDRWKSLHFSGHVAHLEQLIRVRCDENYYSATC 207
QY 166 NKFCPRDFFGHYACDQNGKNTCMGWMGPEC 198
DB 208 NKFCPRDFFGHYTCQYGNKACMDGWMGKEC 240.

RESULT 8
JAG2_RAT
ID JAG2_RAT STANDARD; PRT; 1202 AA.
AC P97607;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Jagged 2 (Jagged2) (Fragment).
GN JAG2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97105852; PubMed=8948600;
RA Shawber C., Boulter J., Lindsell C.E., Weinmaster G.;
RT "Jagged2: a serrate-like gene expressed during rat embryogenesis.";
RL Dev. Biol. 180:370-376(1996).
CC -!- FUNCTION: PUTATIVE NOTCH LIGAND INVOLVED IN THE MEDIATION OF NOTCH
CC SIGNALING. MAY HAVE A ROLE IN NEUROGENESIS IN THE PERIPHERAL
CC NERVOUS SYSTEM, LIMB DEVELOPMENT AND IN THE ADULT BRAIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DEVELOPMENTAL STAGE: AT STAGE E12.5 IT IS DETECTED IN DORSAL ROOT
CC GANGLIA, AER, AND SURFACE ECTODERM. AT E14.5, FOUND AS WELL IN
CC CRANIAL GANGLIA, THYMUS AND OLFACTORY EPITHELIA. AT E16.5, FOUND AS
CC WELL IN SALIVARY GLAND, TOOTH BUDS AND HAIR FOLLICLES.
CC -!- SIMILARITY: Contains 16 EGF-like domains.
CC -!- SIMILARITY: Contains 1 DSL domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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[1]
RN SEQUENCE FROM N.A.
RP STRAIN-Oregon-R;
RX MEDLINE-91347903; PubMed-1840519;
RA Thomas U., Speicher S.A., Knust E.;
RT "The Drosophila gene Serrate encodes an EGF-like transmembrane
RT protein with a complex expression pattern in embryos and wing
RT discs";
RL Development 111:749-761(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-91099666; PubMed-2125287;
RA Fleming R.J., Scottgale T.N., Diederich R.J., Artavanis-Tsakonas S.;
RT "The gene Serrate encodes a putative EGF-like transmembrane protein
RT melanogaster";
RT Development 111:749-761(1991).
RN [3]
RP FUNCTION: ESSENTIAL FOR PROPER ECTODERMAL DEVELOPMENT. SERRATE
CC MAY REPRESENT AN ELEMENT IN A NETWORK OF INTERACTING MOLECULES
CC OPERATING AT THE CELL SURFACE DURING THE DIFFERENTIATION OF
CC CERTAIN TISSUES.
CC -|- TISSUE SPECIFICITY: APPEARS TO BE RESTRICTED EXCLUSIVELY TO
CC CELLS OF ECTODERMAL ORIGIN.
CC -|- MISCELLANEOUS: SEPARATION OF NEUROBLASTS FROM THE ECTODERM INTO
CC THE INNER PART OF EMBRYO IS ONE OF THE FIRST STEPS OF CNS
CC DEVELOPMENT IN INSECTS, THIS PROCESS IS UNDER CONTROL OF THE
CC NEUROGENIC GENES.
CC -|- MISCELLANEOUS: NOTCH AND SERRATE MAY INTERACT AT THE PROTEIN
CC LEVEL, IT IS CONCEIVABLE THAT THE SERRATE AND DELTA PROTEINS MAY
CC COMPETE FOR BINDING WITH THE NOTCH PROTEIN.
CC -|- SIMILARITY: Contains 14 EGF-like domains.
CC -|- SIMILARITY: Contains 1 DSL domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X56811; CAA40148.1; -;
DR EMBL; M35759; AAA28938.1; -;
DR PIR; S16148; S16148.
DR HSP; P00743; 1CCF.
DR FlyBase; FBgn0004197; Ser.
DR GO; GO:0005112; F:Notch binding activity; NAS.
DR GO; GO:0007219; P:N receptor signaling pathway; NAS.
DR GO; GO:0007435; P:salivary gland morphogenesis; NAS.
DR InterPro; IPR00152; Asx_hydroxyl.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006552; VC_out.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 11.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 7.
DR SMART; SM00215; VMC_out; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 7.
DR PROSITE; PS00022; EGF_1; 14.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS01187; EGF_CA; 5.
KW Differentiation; Repeat; EGF-like domain; Transmembrane;
KW Glycoprotein; Signal.
FT SIGNAL 1 83 POTENTIAL.
FT CHAIN 84 1408 SERRATE PROTEIN.
FT DOMAIN 84 1223 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1224 1249 POTENTIAL.

FT DOMAIN 1250 1408 CYTOPLASMIC (POTENTIAL).
FT DSL 221 283
FT DOMAIN 284 317 EGF-LIKE 1.
FT DOMAIN 315 349 EGF-LIKE 2.
FT DOMAIN 351 389 EGF-LIKE 3.
FT DOMAIN 391 489 EGF-LIKE 4.
FT DOMAIN 407 476 SER-RICH (INSERT).
FT DOMAIN 491 527 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 529 609 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 611 646 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 648 684 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 686 721 EGF-LIKE 9.
FT DOMAIN 723 797 EGF-LIKE 10.
FT DOMAIN 737 769 THR-RICH (INSERT).
FT DOMAIN 799 835 EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 837 877 EGF-LIKE 12.
FT DOMAIN 879 915 EGF-LIKE 13.
FT DOMAIN 917 953 EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).
FT DISULFID 288 299 BY SIMILARITY.
FT DISULFID 292 305 BY SIMILARITY.
FT DISULFID 307 316 BY SIMILARITY.
FT DISULFID 319 330 BY SIMILARITY.
FT DISULFID 325 337 BY SIMILARITY.
FT DISULFID 339 348 BY SIMILARITY.
FT DISULFID 355 367 BY SIMILARITY.
FT DISULFID 361 377 BY SIMILARITY.
FT DISULFID 379 388 BY SIMILARITY.
FT DISULFID 395 406 BY SIMILARITY.
FT DISULFID 400 477 BY SIMILARITY.
FT DISULFID 479 488 BY SIMILARITY.
FT DISULFID 495 506 BY SIMILARITY.
FT DISULFID 500 515 BY SIMILARITY.
FT DISULFID 517 526 BY SIMILARITY.
FT DISULFID 533 588 BY SIMILARITY.
FT DISULFID 582 597 BY SIMILARITY.
FT DISULFID 599 608 BY SIMILARITY.
FT DISULFID 615 625 BY SIMILARITY.
FT DISULFID 639 634 BY SIMILARITY.
FT DISULFID 636 645 BY SIMILARITY.
FT DISULFID 652 663 BY SIMILARITY.
FT DISULFID 657 672 BY SIMILARITY.
FT DISULFID 674 683 BY SIMILARITY.
FT DISULFID 690 700 BY SIMILARITY.
FT DISULFID 695 709 BY SIMILARITY.
FT DISULFID 711 720 BY SIMILARITY.
FT DISULFID 803 814 BY SIMILARITY.
FT DISULFID 808 823 BY SIMILARITY.
FT DISULFID 825 834 BY SIMILARITY.
FT DISULFID 841 852 BY SIMILARITY.
FT DISULFID 846 865 BY SIMILARITY.
FT DISULFID 867 876 BY SIMILARITY.
FT DISULFID 883 894 BY SIMILARITY.
FT DISULFID 888 903 BY SIMILARITY.
FT DISULFID 905 914 BY SIMILARITY.
FT DISULFID 921 932 BY SIMILARITY.
FT DISULFID 926 941 BY SIMILARITY.
FT DISULFID 943 952 BY SIMILARITY.
FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 196 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 247 247 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 412 412 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 452 452 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 558 558 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 739 739 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 965 965 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 977 977 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1004 1004 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1030 1030 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1150 1150 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 14 17 MISSING (IN REF. 2).
FT CONFLICT 14 17 P -> A (IN REF. 2).
FT CONFLICT 1352 1352 T -> S (IN REF. 2).

FT DISULFID 276 285 BY SIMILARITY.
FT DISULFID 292 304 BY SIMILARITY.
FT DISULFID 298 314 BY SIMILARITY.
FT DISULFID 316 325 BY SIMILARITY.
FT DISULFID 332 343 BY SIMILARITY.
FT DISULFID 337 352 BY SIMILARITY.
FT DISULFID 354 363 BY SIMILARITY.
FT DISULFID 370 381 BY SIMILARITY.
FT DISULFID 375 391 BY SIMILARITY.
FT DISULFID 393 402 BY SIMILARITY.
FT DISULFID 409 420 BY SIMILARITY.
FT DISULFID 414 429 BY SIMILARITY.
FT DISULFID 431 440 BY SIMILARITY.
FT DISULFID 447 467 BY SIMILARITY.
FT DISULFID 469 478 BY SIMILARITY.
FT DISULFID 485 496 BY SIMILARITY.
FT DISULFID 490 505 BY SIMILARITY.
FT DISULFID 507 516 BY SIMILARITY.
FT CARBOHYD 477 477 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 498 498 E -> Q (IN REF. 2).
FT CONFLICT 502 502 G -> R (IN REF. 4).
FT CONFLICT 510 510 G -> S (IN REF. 2).
SQ SEQUENCE 723 AA; 77956 MW; B4EC455FFA32A12B CRC64;

Query Match 38.6%; Score 431; DB 1; Length 723;
Best Local Similarity 41.3%; Pred. No. 1.1e-32;
Matches 85; Conservative 32; Mismatches 75; Indels 14; Gaps 6;

OY 1 SGOFEILSMONVNGELQNGCC--GGARNPCDRKTRDECCTYFKVCLKEQSVRTAGG 59
DB 22 SCVFELKQEFVFNKGLGNRCRGA--GPPPCA---CRTFFRVCLKHQVSVSEPP 75
OY 60 PCFSFGSTPVIGGNTFNKASRGND--RNRIVLPFSFAMPRSYTLLEVA--WDSSND- 113
DB 76 PCTYSATVPVLGVDSFSLDGGGADSAFNSPIRPFPGFTWPTSTLIEALHTSDPDL 135
OY 114 -TVQDPSIIERASHGMNPSQWOTLKONTGVAHFYQIRVCTDDYGYGFCNKFCRPR 172
DB 136 ATENPERLSRLATQRHLTVGEWSQDLHSGRTDLKYSRVCDEHYGYGCSVFCRPR 195
OY 173 DDFGHYACDQNGKTCHEGWMGPEC 198
DB 196 DDAFGHFTCGERGEKVCNPGMKGPYC 221

RESULT 11
DL_DROME STANDARD; PRT; 833 AA.
AC P10041; Q99108; Q9VDY2;
DT 01-MAR-1989 (Rel. 10, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurogenic locus Delta protein precursor.
GN DL OR CG3619.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RC TISSUE=Embryo;
RA Vaessin H., Bremer K.A., Knust E., Campos-Ortega J.A.;
RT "The neurogenic gene Delta of Drosophila melanogaster is expressed in
RT neurogenic territories and encodes a putative transmembrane protein
RT with EGF-like repeats.";
RL EMBO J. 6:3431-3440(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Oregon-R; TISSUE=Embryo;
RX MEDLINE=89196890; PubMed=3149249;
RA Kocyzyński C.C., Alton A.K., Rehtel K., Kooh P.J., Muskavitch M.A.T.;
RT "Delta, a Drosophila neurogenic gene, is transcriptionally complex and

RT encodes a protein related to blood coagulation factors and epidermal
RT growth factor of vertebrates.";
RL Genes Dev. 2:1723-1735(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.G., Wortman J.R., Randell M.D., Zhang Q., Chen L.A.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Balley R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadeu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosnrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [4]
RP SEQUENCE OF 422-621 FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=87218537; PubMed=3107986;
RA Knust E., Dietrich U., Tepass U., Bremer K.A., Weigel D., Vaessin H.,
RA Campos-Ortega J.A.;
RT "EGF homologous sequences encoded in the genome of Drosophila
RT melanogaster, and their relation to neurogenic genes.";
RL EMBO J. 6:761-766(1987).
RN [5]
RP PATTERN OF TRANSCRIPTION, AND CHARACTERIZATION.
RX MEDLINE=91209246; PubMed=2128477;
RA Haenlin M., Kramatschek B., Campos-Ortega J.A.;
RT "The pattern of transcription of the neurogenic gene Delta of
RT Drosophila melanogaster.";
RL Development 110:905-914(1990).
CC -!- FUNCTION: ESSENTIAL FOR PROPER DIFFERENTIATION OF ECTODERM. DL
CC IS REQUIRED FOR THE CORRECT SEPARATION OF NEURAL AND EPIDERMAL
CC CELL LINESAGES.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: DETECTED IN ALL AREAS WITH NEUROGENIC
CC ABILITIES, FOR EXAMPLE THE NEUROGENIC ECTODERM AND THE PRIMORDIA
CC OF THE SENSE ORGANS. LATER EXPRESSION IS RESTRICTED TO THOSE CELLS
CC THAT HAVE ADOPTED A NEURAL FATE.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY.
CC EXPRESSION IS HIGHEST EARLY IN EMBRYONIC DEVELOPMENT (STAGE 5) AND
CC REDUCES TO A LOW LEVEL DURING LARVAL STAGES.
CC -!- MISCELLANEOUS: SEPARATION OF NEUROBLASTS FROM THE ECTODERM INTO

RA Sakano S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Yoneya T., Tahara T., Nagao K., Yamada Y., Yamamoto T., Miyatani S.,
RA Nishikawa M.;
RL "Molecular cloning of Delta-4, a new mouse and human Notch ligand.";
RT Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 33-685 FROM N.A.
RC TISSUE=Placenta;
RA Mailhos C., Moellich U., Lewis J., Harris A., Bicknell R.,
RA Ish-Horowicz D.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: PLAYS A ROLE IN THE NOTCH SIGNALING PATHWAY. ACTIVATES
CC NOTCH-1 AND NOTCH-4 (BY SIMILARITY).
CC - SUBUNIT: BINDS TO NOTCH-1 AND NOTCH-4 (BY SIMILARITY).
CC - SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC - TISSUE SPECIFICITY: EXPRESSED IN VASCULAR ENDOTHELIUM.
CC - DOMAIN: THE DELTA-SERRATE-LAG2 (DSL) DOMAIN IS REQUIRED FOR
CC BINDING TO THE NOTCH RECEPTOR.
CC - SIMILARITY: Contains 8 EGF-like domains.
CC - SIMILARITY: Contains 1 DSL domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; AF253468; RAF76427.1; -
CC EMBL; AB036931; BAB16085.1; -
CC EMBL; AB043894; BAB18581.1; -
CC EMBL; AF279305; RAB181912.1; -
CC PIR; JC7570; JC7570.
CC HSP; P00740; LEDM.
CC Genew; HGNC:2910; DLL4.
CC MIM; 605185; -
CC GO; GO:0003112; F:Notch binding activity; TAS.
CC GO; GO:0008015; P:circulation; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR00152; ASX_hydroxyl.
CC InterPro; IPR001774; DSL.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_CA.
CC InterPro; IPR001438; EGF_III.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR002049; Laminin_EGF.
CC Pfam; PF01414; DSL; 1.
CC Pfam; PF00008; EGF; 7.
CC PRINTS; PRO0010; EGFBL00D.
CC PRINTS; PRO0011; EGF_LAMININ.
CC SMART; SM00051; DSL; 1.
CC SMART; SM00179; EGF_CA; 2.
CC PROSITE; PS00010; ASX_HYDROXYL; 1.
CC PROSITE; PS00022; EGF_1; 8.
CC PROSITE; PS01186; EGF_2; 7.
KW Signal; EGF-like domain; Repeat; Transmembrane; Developmental protein;
KW Differentiation; Glycoprotein.
FT SIGNAL 1 26
FT CHAIN 27 685
FT DOMAIN 27 529 DELTA-LIKE PROTEIN 4.
FT TRANSMEM 530 550 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 551 685 POTENTIAL.
FT DOMAIN 155 217 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 218 251 DSL.
FT DOMAIN 252 282 EGF-LIKE 1.
FT DOMAIN 284 322 EGF-LIKE 2.
FT DOMAIN 324 360 EGF-LIKE 3.
FT DOMAIN 362 400 EGF-LIKE 4.
FT DOMAIN 400 440 EGF-LIKE 5.

FT DOMAIN 402 438 EGF-LIKE 6.
FT DOMAIN 440 476 EGF-LIKE 7.
FT DOMAIN 480 518 EGF-LIKE 8.
FT DISULFID 222 233 BY SIMILARITY.
FT DISULFID 226 239 BY SIMILARITY.
FT DISULFID 241 250 BY SIMILARITY.
FT DISULFID 253 264 BY SIMILARITY.
FT DISULFID 259 270 BY SIMILARITY.
FT DISULFID 272 281 BY SIMILARITY.
FT DISULFID 288 300 BY SIMILARITY.
FT DISULFID 294 310 BY SIMILARITY.
FT DISULFID 312 321 BY SIMILARITY.
FT DISULFID 328 339 BY SIMILARITY.
FT DISULFID 333 348 BY SIMILARITY.
FT DISULFID 350 359 BY SIMILARITY.
FT DISULFID 366 377 BY SIMILARITY.
FT DISULFID 371 388 BY SIMILARITY.
FT DISULFID 390 399 BY SIMILARITY.
FT DISULFID 406 417 BY SIMILARITY.
FT DISULFID 411 426 BY SIMILARITY.
FT DISULFID 428 437 BY SIMILARITY.
FT DISULFID 444 464 BY SIMILARITY.
FT DISULFID 466 475 BY SIMILARITY.
FT DISULFID 484 495 BY SIMILARITY.
FT DISULFID 489 506 BY SIMILARITY.
FT DISULFID 508 517 BY SIMILARITY.
FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 685 AA; 74604 MW; 6CF89D3C220ACC89 CRC64;

Query Match 37.6%; Score 419.5; DB 1; Length 685;
Best Local Similarity 38.2%; Pred. No. 1.2e-31;
Matches 78; Conservative 40; Mismatches 67; Indels 19; Gaps 5;

QY 1 SQGFLEILSMONVANGELQNGMCCGARNPGRKCTRDCEDTYKVKLCKEYQSRVTAGG 60
DB 27 SGVFQLQLOEFINERGVLASGRPC---EPG-----CRTEFVCLKHQA-VVSPGP 73
QY 61 CSFGSGSTPIVGNTFNK-ASGRNDRNRIVLFPFAMPRSYTLLEAVEADSSNDTVQ--- 116
DB 74 CTFTGTSTPLVLTNSFAVRDSSGGGRNPLQLPFNFTPGTFTSLITEAHAPGDDLPEA 133
QY 117 --PDSLIEKASHSGMINPSROWTKONTGVAHFQYQIRVTCDDYVYFGCKNFCRPRD 174
DB 134 LPDALISKIAIQGSLAVQGNWLLDEQSTLTLRLSYRVICSDNYIGDNCRLCKKRD 193
QY 175 FFGHYACDQNGNKTMEGWMGPEC 198
DB 194 HFGHYVCQPDGNSLCLPGWTGEYC 217

RESULT 13
DLL1_MOUSE
ID DLL1_MOUSE STANDARD; PRT; 722 AA.
AC Q61483;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta).
GN DLL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X BALB/c; TISSUE=Embryo;
RX MEDLINE=95401858; PubMed=7671806;
RA Bettenhausen B., de Angelis M.H., Simon D., Guenet J.-L., Gossler A.;
RT "Transient and restricted expression during mouse embryogenesis of
RT Dll1, a murine gene closely related to Drosophila Delta.";

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2003, 17:50:03 ; Search time 95 Seconds

(without alignments)
537.836 Million cell updates/sec

Title: US-09-995-593A-5

Perfect score: 1116

Sequence: 1 SQCFEILSLMONGELQN.....YACDQNGKTCMEGWGPEC 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTEMBL_23:*

1: sp.archaea:*

2: sp.bacteria:*

3: sp.fungi:*

4: sp.human:*

5: sp.invertebrate:*

6: sp.mammal:*

7: sp.mhc:*

8: sp.organelle:*

9: sp.phage:*

10: sp.plant:*

11: sp.podent:*

12: sp.virus:*

13: sp.vertebrate:*

14: sp.unclassified:*

15: sp.rvirus:*

16: sp.bacteriap:*

17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	973	87.2	1193	13	Q90819
2	947	84.9	1214	13	Q90YD2
3	722.5	64.7	1212	13	Q42347
4	671.5	60.2	1216	13	Q90Y55
5	671.5	60.2	1254	13	Q90Y56
6	665.5	59.6	1254	13	Q9YHU2
7	446	40.0	1404	5	Q9VB65
8	433.5	38.8	728	13	Q90656
9	420	37.6	721	13	Q91902
10	413	37.0	717	13	P87357
11	412	36.9	720	13	Q8UWJ4
12	410.5	36.8	686	11	Q90BU9
13	401.5	36.0	836	13	Q8AW87
14	396.5	35.5	807	5	Q8MP01
15	395.5	35.4	802	13	O57462
16	359	32.2	684	5	Q81498

17	351	31.5	721	5	Q95YG0
18	338.5	30.3	615	13	O57409
19	332	29.7	642	13	P79941
20	322.5	28.9	674	5	Q8TAN9
21	318	28.5	664	13	Q9IAT6
22	305	27.3	438	5	Q8I497
23	293.5	26.3	794	5	Q8TAP0
24	285.5	25.6	139	11	P97606
25	236.5	21.2	185	5	O8WQ03
26	187	16.8	587	4	Q8NBS4
27	173	15.5	950	5	Q8MQN5
28	127	11.4	144	13	O12973
29	125.5	11.2	379	5	Q19922
30	124.5	11.2	349	5	Q17377
31	111	9.9	252	5	O45201
32	100	9.0	864	11	O8C720
33	94	8.4	718	5	Q9BI07
34	93	8.3	809	11	O8CA82
35	92.5	8.3	488	4	O8N504
36	92.5	8.3	491	4	Q8TB07
37	90.5	8.1	510	4	Q9H4V1
38	90	8.1	1270	5	Q9GPN0
39	89.5	8.0	454	5	O8I709
40	89	8.0	406	5	Q25059
41	87.5	7.8	225	5	Q8T2M9
42	87.5	7.8	434	5	Q9W0A0
43	87.5	7.8	553	13	O8AW56
44	87.3	7.8	2653	5	Q25253
45	86	7.7	823	11	Q8R3D3

ALIGNMENTS

RESULT 1

Q90819	ID	Q90819	PRELIMINARY:	PRT;	1193 AA.
AC	Q90819;				
DT	01-NOV-1996	(T-EMBLrel. 01, Created)			
DT	01-NOV-1996	(T-EMBLrel. 01, Last sequence update)			
DT	01-MAR-2003	(T-EMBLrel. 23, Last annotation update)			
DE	C-Serate-1 protein (Fragment).				
OS	Gallus gallus (Chicken).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;				
OC	Gallus.				
OX	NCBI_TaxID=9031;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Otic explant;				
RX	MEDLINE=96175595; PubMed=8631496;				
RA	Myat A., Henrique D., Ish-Horowicz D., Lewis J.;				
RT	"A chick homologue of Serrate and its relationship with Notch and				
RL	Dev. Biol. 174:233-247(1996).				
DR	EMBL; X95283; CAA64604.1; -				
DR	HSSP; P00740; IEDM.				
DR	InterPro; IPR000152; Asx_hydroxyl.				
DR	InterPro; IPR001774; DSL.				
DR	InterPro; IPR000742; EGF_2.				
DR	InterPro; IPR001881; EGF_Ca.				
DR	InterPro; IPR001438; EGF_II.				
DR	InterPro; IPR006209; EGF_like.				
DR	InterPro; IPR001007; VWF_C.				
DR	Pfam; PF01414; DSL; 1.				
DR	Pfam; PF00008; EGF; 14.				
DR	PRINTS; PR00010; EGFBL00.				
DR	SMART; SM00051; DSL; 1.				
DR	SMART; SM00179; EGF_CA; 10.				
DR	SMART; SM00214; VWC; 1.				
DR	PROSITE; PS00010; ASX_HYDROXYL; 10.				
DR	PROSITE; PS00022; EGF_1; 16.				
DR	PROSITE; PS01186; EGF_2; 12.				

Q95Y00	ciona savi
O57409	brachydanio
P79941	xenopus lae
Q8T4N9	strongyloce
Q9IAT6	brachydanio
Q8I497	cupiennius
Q8T4P0	lytechinus
P97606	rattus norv
O8WQ03	calliphora
Q8NBS4	homo sapien
Q8MQN5	drosohilla
O12973	gallus gall
Q19922	caenorhabdi
Q17377	caenorhabdi
O45201	caenorhabdi
O8C720	mus musculu
Q9BI07	entamoeba h
O8CA82	mus musculu
Q8N504	homo sapien
Q8TB07	homo sapien
Q9H4V1	homo sapien
Q9GPN0	caenorhabdi
Q8I709	trypanosoma
Q25059	heliocidari
Q8T2M9	dictyosteli
Q9W0A0	drosohilla
O8AW56	brachydanio
Q25253	lucilia cup
Q8R3D3	mus musculu

DR PROSITE; PS01187; EGF_CA; 8.
KW EGF-like domain.
FT NON_TER 1
SQ SEQUENCE 1193 AA; 131039 MW; 24E94D09EB987935 CRC64;

Query Match 87.2%; Score 973; DB 13; Length 1193;
Best Local Similarity 85.4%; Pred. No. 3.8e-89;
Matches 169; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 SQQFELEILSMQNVNGLONGNCCGARNPGDRKCTRDCEDTYFKVCLKEYQSRVTAGGP 60
DB 6 SQQFEILSVQNVNGLONGNCCDGTNRNPGDKCTRDCEDTYFKVCLKEYQSRVTAGGP 65

QY 61 CSFGSGSTPVIGNTFNKASRGNDNRNRLVLPFSFAWPRSYTLVVEAWDSSNDTVQPSI 120
DB 66 CSFGSKSTPVIGNTFNKYSRNNENRNLVLPFSFAWPRSYTLVVEAWDYNDSNPDR 125

QY 121 IEKASHGMINPSROWQTLKQNTGVAHFYQIRVTCDDYYVFGCNKFCRPRDDFFGHYA 180
DB 126 IEKASHGMINPSROWQTLKHTGAHFYQIRVTCDEHYVFGCNKFCRPRDDFFHT 185

QY 181 CDQNGKTCMEGWMGPEC 198
DB 186 CDQNGKTCLEGTGPEC 203

RESULT 2

ID Q90YD2 PRELIMINARY; PRT; 1214 AA.
AC Q90YD2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE X-Serrate-1 protein.
GN X-SERRATE-1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21541033; PubMed=11685570;
RA Kiyota T., Jono H., Kuriyama S., Hasegawa K., Miyatani S.,
RA Kinoshita T.;
RT "X-Serrate-1 is involved in primary neurogenesis in Xenopus laevis in
a complementary manner with X-Delta-1.";
RL Dev. Genes Evol. 211:367-376(2001).
DR EMBL; AB027537; BAB59049.1; -
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 14.
DR PRINTS; PR00010; EGF_BLOOD.
DR PRINTS; PR00011; EGF_FLAMININ.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 10.
DR SMART; SM00214; VWC_1.
DR PROSITE; PS00010; ASX_HYDROXYL; 10.
DR PROSITE; PS00022; EGF_1; 16.
DR PROSITE; PS01186; EGF_2; 12.
DR PROSITE; PS01187; EGF_CA; 8.
KW EGF-like domain.
SQ SEQUENCE 1214 AA; 133807 MW; A9C09C420CC157C2 CRC64;

Query Match 84.9%; Score 947; DB 13; Length 1214;
Best Local Similarity 82.8%; Pred. No. 1.6e-86;

Matches 164; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 SQQFEILSMQNVNGLONGNCCGARNPGDRKCTRDCEDTYFKVCLKEYQSRVTAGGP 60
DB 28 SQQFEILSMQNVNGLONGNCCDGTNRNPGDKCTRDCEDTYFKVCLKEYQSRVSAGGA 87

QY 61 CSFGSGSTPVIGNTFNKASRGNDNRNRLVLPFSFAWPRSYTLVVEAWDSSNDTVQPSI 120
DB 88 CSFGGYTPVIGNSFNKYSRNNENRNLVLPFSFAWPRSYTLVVEAWDYNNDTNDPGDL 147

QY 121 IEKASHGMINPSROWQTLKQNTGVAHFYQIRVTCDDYYVFGCNKFCRPRDDFFGHYA 180
DB 148 IEKASHGMINPSROWQTLKQNTGVAHFYQIRVTCDEHYVFGCNKFCRPRDDFFGHYT 207

QY 181 CDQNGKTCMEGWMGPEC 198
DB 208 CDQNGKTCLEGTGPEC 225

RESULT 3

O42347
ID O42347 PRELIMINARY; PRT; 1212 AA.
AC O42347;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE C-serrate-2 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97184054; PubMed=9032014;
RA Hayashi H., Mochii M., Kodama R., Hamada Y., Mizuno N., Eguchi G.,
RA Tachi C.;
RT "Isolation of a novel chick homologue of Serrate and its coexpression
with C-Notch-1 in chick development.";
RL Int. J. Dev. Biol. 40:1089-1096(1996).
DR EMBL; D87558; BAA21713.1; -
DR HSP; P01132; IEGF.
DR InterPro; IPR00152; Asx_hydroxyl.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 14.
DR PRINTS; PR00010; EGF_BLOOD.
DR PRINTS; PR00011; EGF_FLAMININ.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 10.
DR SMART; SM00214; VWC_1.
DR PROSITE; PS00010; ASX_HYDROXYL; 10.
DR PROSITE; PS00022; EGF_1; 16.
DR PROSITE; PS01186; EGF_2; 10.
DR PROSITE; PS01187; EGF_CA; 8.
KW EGF-like domain.
FT NON_TER 1
SQ SEQUENCE 1212 AA; 134188 MW; BC44D29F1C7985FE CRC64;

Query Match 64.7%; Score 722.5; DB 13; Length 1212;
Best Local Similarity 62.0%; Pred. No. 7e-64;
Matches 127; Conservative 26; Mismatches 45; Indels 7; Gaps 2;

QY 1 SQQFEILSMQNVNGLONGNCCGARNPGDRKCTRDCEDTYFKVCLKEYQSRVTAGGP 60
DB 6 TGYFELQNSRVNNGELNGECDDGERNPPDRDGRDCEDTYFKVCLKEYQAKISPGGP 65

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Qy 61 CSFGSGTPVIGGNTFNKA-----SRGNDNRNRLVLPFFAWPRSYTLLEAVDSSNDT 114
Db 66 CSYGGSTPVLGGNLYLNGDKYHPRGSRPETSGRIVIPFOYAWPRSTLLEAWDNDT 125
Qy 115 VQ-PDSIIKASHSGMNPBROWQTLKQNTGVAHFQIRVTCDDYYGFCNKFQRPD 173
Db 126 KSGEDLLIERVAHAGMNPEDRWKTLQFNPGVAFVQIRVCDENYISALCNKFCGPRD 185
Qy 174 DFFGHYACDQNGKNTMEGWMGPEC 198
Db 186 DFFGHYTCQNGNKACMEGWMGPEC 210

RESULT 4
Q90Y55 PRELIMINARY; PRT; 1216 AA.
AC Q90Y55;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Jagged2.
GN JAG2.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Oda T., Chandrasekharappa S.C.;
RT "Isolation, Characterization and Expression Analysis of Zebrafish
RT Jagged Genes.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF229450; AAL08215.1; -.
DR ZFIN; ZDB-GENE-011128-3; jag2.
DR InterPro; IPR000152; ASX_hydroxyl.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 15.
DR Pfam; PF00093; vwc; 1.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 8.
DR SMART; SM00214; VWC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 6.
DR PROSITE; PS00022; EGF_1; 15.
DR PROSITE; PS01186; EGF_2; 10.
DR PROSITE; PS01187; EGF_CA; 5.
KW EGF-like domain.
SQ SEQUENCE 1216 AA; 133616 MW; A654A171EAB011AB CRC64;

Query Match 60.2%; Score 671.5; DB 13; Length 1216;
Best Local Similarity 55.6%; Pred. No. 9.8e-59;
Matches 114; Conservative 35; Mismatches 49; Indels 7; Gaps 2;

Qy 1 SGOFELILSMQNVNGLONGCCGARNPGDKRCKTRDECDTYFKVCLKEYQSRVTAGG 60
Db 28 SGYFELQLIAVENVNGELWGECCDSTRNSQDQRCVRDECDTYFKVCLKEYQSEVTTGQ 87
Qy 61 CSFGSGTPVIGGNTFNKA-----SRGNDNRNRLVLPFFAWPRSYTLLEAVDSSNDT 115
Db 88 CTFGSGSTDLVGGNIFSKTAKNSPKSTSDVGKIIIPFHEAWPRSYTLLEAWDNDSTQ 147
Qy 116 Q--PDSIIKASHSGMNPBROWQTLKQNTGVAHFQIRVTCDDYYGFCNKFQRPD 173
Db 148 NNGEENLIERHIIASHVNPBGDHWQSIHPIGTAHIEYRIVRCDENYIGSKNKCQCRPD 207
Qy 174 DFFGHYACDQNGKNTMEGWMGPEC 198
Db 208 DFFGHYKCDPSGNIVCLDGNMGEDC 232

RESULT 6
Q9YHU2 PRELIMINARY; PRT; 1254 AA.
AC Q9YHU2
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)

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Db 208 DYFGHYRCDPSGNIVCLDGNMGEDC 232

RESULT 5
Q90Y56 PRELIMINARY; PRT; 1254 AA.
AC Q90Y56;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Jagged2.
GN JAG2.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Oda T., Chandrasekharappa S.C.;
RT "Isolation, Characterization and Expression Analysis of Zebrafish
RT Jagged Genes.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF229449; AAL08214.1; -.
DR ZFIN; ZDB-GENE-011128-3; jag2.
DR InterPro; IPR000152; ASX_hydroxyl.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 15.
DR Pfam; PF00093; vwc; 1.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 8.
DR SMART; SM00214; VWC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 7.
DR PROSITE; PS00022; EGF_1; 16.
DR PROSITE; PS01186; EGF_2; 11.
DR PROSITE; PS01187; EGF_CA; 6.
KW EGF-like domain.
SQ SEQUENCE 1254 AA; 137719 MW; AFF70717DF190FEB CRC64;

Query Match 60.2%; Score 671.5; DB 13; Length 1254;
Best Local Similarity 55.6%; Pred. No. 1e-58;
Matches 114; Conservative 35; Mismatches 49; Indels 7; Gaps 2;

Qy 1 SGOFELILSMQNVNGLONGCCGARNPGDKRCKTRDECDTYFKVCLKEYQSRVTAGG 60
Db 28 SGYFELQLIAVENVNGELWGECCDSTRNSQDQRCVRDECDTYFKVCLKEYQSEVTTGQ 87
Qy 61 CSFGSGTPVIGGNTFNKA-----SRGNDNRNRLVLPFFAWPRSYTLLEAVDSSNDT 115
Db 88 CTFGSGSTDLVGGNIFSKTAKNSPKSTSDVGKIIIPFHEAWPRSYTLLEAWDNDSTQ 147
Qy 116 Q--PDSIIKASHSGMNPBROWQTLKQNTGVAHFQIRVTCDDYYGFCNKFQCRPD 173
Db 148 NNGEENLIERHIIASHVNPBGDHWQSIHPIGTAHIEYRIVRCDENYIGSKNKCQCRPD 207
Qy 174 DFFGHYACDQNGKNTMEGWMGPEC 198
Db 208 DYFGHYKCDPSGNIVCLDGNMGEDC 232

RESULT 6
Q9YHU2 PRELIMINARY; PRT; 1254 AA.
AC Q9YHU2
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)

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RESULT 11
Q8UWJ4      PRELIMINARY;          PRT;    720 AA.
AC   Q8UWJ4;
DT   01-MAR-2003 (TREMBlrel. 20, Created)
DT   01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT   01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE     Deltad protein.
OS   Brachydanio rerio (Zebrafish). (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
CC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
[1]
RP   SEQUENCE FROM N.A.
RA   Hans S., Campos-Ortega J.A.;
RT   "On the organization of the regulatory region of the zebrafish deldad gene.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF426384; AAL31528.1; -
DR   InterPro; IPR000152; Asx_hydroxyl.
DR   InterPro; IPR001774; DSL.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR001881; EGF_CA.
DR   InterPro; IPR001438; EGF-II.
DR   InterPro; IPR006209; EGF-like.
DR   InterPro; IPR002049; Laminin_EGF.
DR   Pfam; PF01414; DSL; 1.
DR   Pfam; PF00008; EGF; 8.
DR   PRINTS; PRO00010; EGFBLOOD.
DR   SMART; PR00011; EGLAMININ.
DR   SMART; SM00051; DSL; 1.
DR   SMART; SM00179; EGF_CA; 4.
DR   ProSITE; PS00010; ASX_HYDROXYL; 3.
DR   ProSITE; PS00022; EGF_1; 8.
DR   ProSITE; PS01186; EGF_2; 8.
DR   ProSITE; PS01187; EGF_CA; 2.
KW   EGF-like domain.
SQ   SEQUENCE       720 AA;  79380 MW;  DE6B7393E2AA0FE6 CRC64;

Query Match           36.9%; Score 412; DB 13; Length 720;
Best Local Similarity 38.7%; Pred.No. 7.5e-33;
Matches 79; Conservative 33; Mismatches 82; Indels 10; Gaps 5

Qy   1 SGQELETLSMNYNGELQNCGGARNPGDKCTRDECPTYFKVCLKEYQSRYTAGGP 60
Db   | ||||| : | | | | : | | | | : | | | | | | | | : |
        20 SGVEFLKLQLPLNKKGYGTGNANCKGSAAEG-HQC---ECKTFRICLKHYQANYSPDP 75
        | ||||| : | | | | : | | | | : | | | | | | | | : |
Qy   61 CSFGSGSTPVIGNTFNLIKAS--RGNDNRNIVLPFSFAMPRSYTLLVERA--WDSSND--T 114
Db   | ||||| : | | | | : | | | | : | | | | | | | | : |
        76 CTYGAVTPVLGNSFQPVDPSFTNPFPAGFTWPGETPGLSLIEALHTSDDDLST 135
        | ||||| : | | | | : | | | | : | | | | | | | | : |
Qy   115 VQPSIITEKASHSMINPSROWOTLKONTGAHPEYQIRVTCDYYGGCNCNKFCRRDD 174
Db   | ||||| : | | | | : | | | | : | | | | | | | | : |
        136 ENPDRIISRMTQRHLTVGEWSODLOVGGRTELKYSYRFVCDEHIYEGCSVFRCRRDD 195
        | ||||| : | | | | : | | | | : | | | | | | | | : |
Qy   175 FFGHVACDONGNKTCEMGWMGPC 198
Db   | ||||| : | | | | : | | | | : | | | | | | | | : |
        196 TFGHFTCGERGEIIICNSGWKGQYC 219
        | ||||| : | | | | : | | | | : | | | | | | | | : |


RESULT 12
Q9DBU9      PRELIMINARY;          PRT;    686 AA.
AC   Q9DBU9;
DT   01-JUN-2001 (TREMBlrel. 17, Created)
DT   01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT   01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE     Delta-like 4 homolog (Drosophila).
DS   DLL4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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